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OM protein - protein search, using sw model

Run on: September 21, 2005, 11:47:33 ; Search time 89 Seconds  
(without alignments)  
2216.267 Million cell updates/sec

Title: US-09-807-660C-2

Perfect score: 2698  
Sequence: 1 MEDTKESNVKTFCSKNILAI.....VAIIGLLIHFHKPSYFWKDMV 510

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003s:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2698	100.0	510	2	AAW04334 Human lym
2	2698	100.0	510	2	AAW04264 Human CD3
3	2698	100.0	510	3	AAV70910 Human sol
4	2698	100.0	510	3	AAV70887 Human sol
5	2698	100.0	510	4	AAV70917 Human CD3
6	2698	100.0	510	7	ADJ57262 Human CD3
7	2698	100.0	510	8	ADL24295 Human CD3
8	2698	100.0	510	8	ADQ9453 Human CD3
9	2698	100.0	510	8	ADR69210 Human CD3
10	2698	100.0	510	8	ADR69042 Human CD3
11	2698	100.0	510	8	ADSL17924 Human CD3
12	2698	100.0	510	8	ABO84674 Human can
13	2698	100.0	510	8	ADR87821 Human CD3
14	2698	100.0	511	8	ADK60421 Angiogene
15	2698	100.0	511	8	ADK60722 Angiogene
16	2698	100.0	511	8	ADP73345 CD39 lymph
17	2677	99.2	517	7	ADN95839 Human BEC
18	2677	99.2	517	8	ADK60221 Angiogene
19	2677	99.2	517	8	ADK60522 Angiogene
20	2677	99.2	517	8	ADP73145 Angiogene
21	2673	99.1	522	8	ABO84672 Human can
22	2469	91.5	529	8	ABM83376 Human dia
23	2358	87.4	464	3	AAV70922 Human sol
24	2358	87.4	464	3	AAV70899 Protein e
25	2348	87.0	439	4	AAV71918 Soluble h

26	2348	87.0	454	3	AAV70913 Human sol
27	2348	87.0	454	3	AAV70890 Protein e
28	2348	87.0	463	3	AAV70925 Human sol
29	2348	87.0	463	3	AAV70902 Protein e
30	2348	87.0	473	3	AAV70924 Human sol
31	2348	87.0	473	3	AAV70901 Protein e
32	2348	87.0	474	3	AAV70923 Human sol
33	2348	87.0	474	3	AAV70900 Protein e
34	2348	87.0	476	3	AAV70911 Human CD3
35	2348	87.0	476	3	AAV70888 Protein e
36	2348	87.0	478	3	AAV70914 Human sol
37	2348	87.0	478	3	AAV70891 Protein e
38	2348	87.0	487	3	AAV70921 Human sol
39	2348	87.0	487	3	AAV70898 Protein e
40	2311	85.7	503	8	ABM83377 Human dia
41	2297	85.1	476	3	AAV70912 Human CD3
42	2297	85.1	476	3	AAV70889 Protein e
43	2144	79.5	402	8	ABO84671 Human can
44	2016	74.7	377	7	ADI62735 Human apo
45	1293	47.9	311	8	ABO84673 Human can

ALIGNMENTS

RESULT 1  
AAW04334  
ID AAW04334 standard; protein; 510 AA.  
AC AAW04334;  
XX  
XX 29-DEC-1996 (first entry)  
XX Human lymphoid cell activation antigen CD39.  
DE  
XX ATP diphosphohydrolase; ATPDase; bovine aorta; pig pancreas; apyrase;  
KW CD39; lymphoid cell activation antigen; enzyme; platelet aggregation;  
KW thrombogenicity; anti-haemostatic.  
XX  
OS Homo sapiens.  
XX  
XX WO9632471-A2.  
XX  
XX 17-OCT-1996.  
XX  
XX 10-APR-1996; 96WO-CA000223.  
XX  
XX 10-APR-1995; 95US-00419204.  
XX (UYSH ) UNIV SHERBROOKE.  
XX Beaudoin AR, Sevigny J;  
XX WPI, 1996-477122/47.  
XX N-PSDB; AAT38516.  
XX Isolated ATP di-phospho-hydrolase enzymes - have anti-haemostatic activity, useful for reducing platelet aggregation and thrombogenicity.  
XX Claim 17; Page 42-44; 60pp; English.  
XX The bovine aorta (AAW04335 and AAW04338 and AAW04340) and porcine pancreatic (AAW04339) ATPDases have been partially sequenced. The sequences have been found to be highly homologous to a human lymphoid cell activation antigen designated CD39 (Maliszewski et al. (1994). J. Immunol.: 3574-3583). The complete sequences of the ATPDases types I and II have not been obtained yet. Assuming that the CD39 gene product is an ATPDase type II, the use of CD39 in the reduction of platelet aggregation and of thrombogenicity may be contemplated, as well as a process of making ATPDases using the CD39 sequence (AAT38516)

Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 2; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVTFCCKNLAIFGSSIIAVIALAVGLTQNKALPENVKYGVILDDAGSSHT 60  
DB 1 MEDTKESNVTFCCKNLAIFGSSIIAVIALAVGLTQNKALPENVKYGVILDDAGSSHT 60

QY 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKVFQVNEIGIYLTDCMERAREVIPSQ 120  
DB 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKVFQVNEIGIYLTDCMERAREVIPSQ 120

QY 121 HQETPVYLGATAGMRLRMESEBELADRVLDVVERSLSNYPFDQGARIIITGOEGAYGWI 180  
DB 121 HQETPVYLGATAGMRLRMESEBELADRVLDVVERSLSNYPFDQGARIIITGOEGAYGWI 180

QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPPQNQTIESPDNALQFR 240  
DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPPQNQTIESPDNALQFR 240

QY 241 LYGKDYNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCPHPGYKKVNVNVDLYKTP 300  
DB 241 LYGKDYNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCPHPGYKKVNVNVDLYKTP 300

QY 301 CTKRFEMTLPFQOFIEQIGNYQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360  
DB 301 CTKRFEMTLPFQOFIEQIGNYQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360

QY 361 SAFYFVWKFLNLTSEKVSQEKVTEMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420  
DB 361 SAFYFVWKFLNLTSEKVSQEKVTEMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420

QY 421 SLLQGYHFTADSWEHIFGKIQGSADAGWTLYGMLNLTNMIAPAEQPLSTPLSHSYVFL 480  
DB 421 SLLQGYHFTADSWEHIFGKIQGSADAGWTLYGMLNLTNMIAPAEQPLSTPLSHSYVFL 480

QY 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510  
DB 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 2  
AAW04264  
ID AAW04264 standard; protein; 510 AA.

AC AAW04264;  
XX  
XX 29-MAY-1997 (first entry)  
XX  
XX Human CD39 protein.  
XX  
XX Human; lymphocyte activation marker; gene therapy;  
XX ATP diphosphohydrolase; transgenic animal; pig; porcine; graft; donor;  
XX transplantation; endothelial cell; prosthetic device;  
XX platelet aggregation; inhibition; intravascular.

XX Homo sapiens.  
XX WO9630532-A1.  
XX  
XX 03-OCT-1996.  
XX  
XX 22-MAR-1996; 96WO-EP001270.  
XX  
XX 24-MAR-1995; 95US-00410371.  
XX  
XX 12-FEB-1996; 96US-00600383.  
XX  
XX (SANO ) SANDOZ LTD.  
XX (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.  
XX  
XX Bach FH, Robson S;  
XX  
XX WPI; 1996-455377/45.

DR N-PSDB; AAT33966.  
XX Gene therapy of inflammatory or immunological stimulation of platelet  
PT aggregation - using CD39 protein with AIP di:phospho:hydrolase activity,  
PT useful for preventing or alleviating thrombotic condition in mammalian  
PT subject.  
XX  
XX Claim 3; Page 39; 65pp; English.  
XX  
XX Non-human transgenic or somatic recombinant mammals, whose cells contain  
CC a heterologous DNA encoding a polypeptide (especially human CD39 protein)  
CC having ATP-diphosphohydrolase activity under cellular activating  
CC conditions is claimed. In particular the animal is a pig and its cells  
CC (or tissues or organs) can be used for transplantation. DNA coding for  
CC human CD39 is also useful for genetically modifying a mammalian cell to  
CC render it less susceptible to an inflammatory or immunological stimulus  
CC and platelet aggregation. The modified cells can be used to prevent or  
CC alleviate a thrombotic condition. The present sequence is that of the  
CC human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-  
CC 3584

SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 2; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVTFCCKNLAIFGSSIIAVIALAVGLTQNKALPENVKYGVILDDAGSSHT 60  
DB 1 MEDTKESNVTFCCKNLAIFGSSIIAVIALAVGLTQNKALPENVKYGVILDDAGSSHT 60

QY 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKVFQVNEIGIYLTDCMERAREVIPSQ 120  
DB 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKVFQVNEIGIYLTDCMERAREVIPSQ 120

QY 121 HQETPVYLGATAGMRLRMESEBELADRVLDVVERSLSNYPFDQGARIIITGOEGAYGWI 180  
DB 121 HQETPVYLGATAGMRLRMESEBELADRVLDVVERSLSNYPFDQGARIIITGOEGAYGWI 180

QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPPQNQTIESPDNALQFR 240  
DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPPQNQTIESPDNALQFR 240

QY 241 LYGKDYNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCPHPGYKKVNVNVDLYKTP 300  
DB 241 LYGKDYNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCPHPGYKKVNVNVDLYKTP 300

QY 301 CTKRFEMTLPFQOFIEQIGNYQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360  
DB 301 CTKRFEMTLPFQOFIEQIGNYQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360

QY 361 SAFYFVWKFLNLTSEKVSQEKVTEMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420  
DB 361 SAFYFVWKFLNLTSEKVSQEKVTEMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420

QY 421 SLLQGYHFTADSWEHIFGKIQGSADAGWTLYGMLNLTNMIAPAEQPLSTPLSHSYVFL 480  
DB 421 SLLQGYHFTADSWEHIFGKIQGSADAGWTLYGMLNLTNMIAPAEQPLSTPLSHSYVFL 480

QY 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510  
DB 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 3  
AAW70910  
ID AAW70910 standard; protein; 510 AA.

XX  
XX AAW70910;  
XX  
XX 17-AUG-2000 (first entry)  
XX  
XX Human soluble CD39 protein.



FT	/note= "Aen is N-glycosylated"	
FT	292..294	
FT	/note= "Aen is N-glycosylated"	
FT	334..336	
FT	/note= "Aen is N-glycosylated"	
FT	371..373	
FT	/note= "Aen is N-glycosylated"	
FT	457..459	
FT	/note= "Aen is N-glycosylated"	
FT	477..499	
FT	/label= Transmembrane_domain	
XX		
PN	W0200023094-A2.	
XX		
PD	27-APR-2000.	
XX		
XX	13-OCT-1999; 99WO-US023641.	
XX		
PR	16-OCT-1998; 98US-0104585P.	
PR	06-NOV-1998; 98US-0107466P.	
PR	13-AUG-1999; 99US-0149010P.	
XX		
PA	(IMMV ) IMMUNEX CORP.	
PA	(CORR ) CORNELL RES FOUND INC.	
XX		
PI	Maliszewski CR, Gayle RB, Marcus AJ;	
XX		
DR	WPI; 2000-339518/29.	
DR	N-PSDB; AAD00200.	
XX		
XX	Inhibiting platelet activation and recruitment, useful for treating a	
PT	mammal suffering from unstable angina, myocardial infarction, stroke	
PT	coronary artery disease or injury, comprises administering soluble CD39	
PT	polypeptides.	
XX		
PS	Claim 2; Fig 1; 118pp; English.	
XX		
CC	The present sequence is soluble CD39 having apyrase activity. Soluble	
CC	CD39 retains the capacity of wildtype CD39 to metabolise ATP and ADP at	
CC	physiologically relevant concentrations as well as the ability to block	
CC	and reverse ADP-induced platelet activation and recruitment including	
CC	platelet aggregation. This is used in the treatment of unstable angina,	
CC	myocardial infarction, stroke, coronary artery disease or injury.	
CC	atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism,	
CC	platelet-associated ischaemic disorder including lung ischaemia, coronary	
CC	ischaemia and cerebral ischaemia, thrombotic disorder including coronary	
CC	artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,	
CC	peripheral artery thrombosis, venous thrombosis, thrombosis,	
CC	coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),	
CC	transient ischaemic attack. Soluble CD39 is also useful for preventing	
CC	thrombus formation or reformation, occlusion, reocclusion, stenosis or	
CC	restenosis of blood vessels or stroke	
XX		
SQ	Sequence 510 AA;	
	Query Match 100.0%; Score 2698; DB 3; Length 510;	
	Best Local Similarity 100.0%; Pred. No. 5.2e-262;	
	Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MEDTKSNVKTFCNKILALGFSSIIAVIALLAGLTQNKALPENVKYGVILDAGSSHT 60	
DB	1 MEDTKSNVKTFCNKILALGFSSIIAVIALLAGLTQNKALPENVKYGVILDAGSSHT 60	
QY	61 SLVIYKPAEKENDTGTVHQBVECRVKGPGISKVFQKWEIGIYLTDCMERAREVTPRSQ 120	
DB	61 SLVIYKPAEKENDTGTVHQBVECRVKGPGISKVFQKWEIGIYLTDCMERAREVTPRSQ 120	
QY	121 HQSTPYVLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEEGAYGWI 180	
DB	121 HQSTPYVLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEEGAYGWI 180	
QY	181 TINYLKGFQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQNQTIESPDNALQFR 240	

Db	181	TINYLKGFQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQNQTIESPDNALQFR	240
QY	241	LYGKDYNYVTHSFLCYGKQDQALWOKLAXDIOVASNEILRDPCHFPGYKVVNVSDLYKTP	300
Db	241	LYGKDYNYVTHSFLCYGKQDQALWOKLAXDIOVASNEILRDPCHFPGYKVVNVSDLYKTP	300
QY	301	CTKRFEWTLPFQOQFEIQIGIGNYQQCHQSILELNFNTSYCPYSQCAFNGIFLPLPQGDGAF	360
Db	301	CTKRFEWTLPFQOQFEIQIGIGNYQQCHQSILELNFNTSYCPYSQCAFNGIFLPLPQGDGAF	360
QY	361	SAPYFVMKFLNLTSEKVSQEKVTMMKKPCAQPMBEIKTSYAGVKEKYUSEYCFSGSTYIL	420
Db	361	SAPYFVMKFLNLTSEKVSQEKVTMMKKPCAQPMBEIKTSYAGVKEKYUSEYCFSGSTYIL	420
QY	421	SLLLQGYHFTADSWEHIFIGIKIQGSDAGWTLYGMLNTNMIPAEQPLSTPLSHSTYVFL	480
Db	421	SLLLQGYHFTADSWEHIFIGIKIQGSDAGWTLYGMLNTNMIPAEQPLSTPLSHSTYVFL	480
QY	481	MVLSLVLTVAIIIGLLIFPHKPSYFWKDMV	510
Db	481	MVLSLVLTVAIIIGLLIFPHKPSYFWKDMV	510
	RESULT 5		
	AAB71917		
ID	AAB71917	standard; protein; 510 AA.	
XX	AC	AAB71917;	
DT	09-MAY-2001	(first entry)	
XX	DE	Human CD39.	
XX	KW	Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;	
XX	OS	stroke; thrombotic disorder; ischaemic disorder.	
XX	PN	Homo sapiens.	
XX	PD	WO200111949-A1.	
XX	PF	22-FEB-2001.	
XX	PR	11-AUG-2000; 2000WO-US022060.	
XX	PA	13-AUG-1999; 99US-00374586.	
XX	PI	(UYCO ) UNIV COLUMBIA NEW YORK.	
XX	DR	Pinsky DJ;	
XX	DR	WPI; 2001-202805/20.	
PT	Treating stroke in a subject susceptible to intracranial hemorrhaging and		
PT	an ischemic disorder, involves administering a CD39 polypeptide which		
PT	inhibits ADP-mediated platelet aggregation or leukocyte accumulation.		
PS	Claim 1; Page 14; 118pp; English.		
CC	The present sequence is the human CD39 polypeptide. The present sequence		
CC	or its active fragment may be administered to treat or prevent stroke in		
CC	a subject susceptible to intracranial haemorrhaging or an ischaemic		
CC	disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation		
CC	or leukocyte accumulation and/or ATP by increasing ADP catabolism to the		
CC	subject. It is useful for treating or preventing stroke, thrombotic		
CC	disorders and ischaemic disorders such as peripheral vascular disorder,		
CC	pulmonary embolus, venous thrombosis, myocardial infarction, transient		
CC	ischaemic attack, unstable angina, reversible ischaemic neurological		
CC	deficit and sickle cell anaemia. It is also useful for treating or		
CC	preventing a stroke disorder in a subject undergoing heart surgery, lung		
CC	surgery, spinal surgery, brain surgery, vascular surgery, abdominal		
XX	surgery, or organ transplantation surgery		
SQ	Sequence 510 AA;		



Query Match 100.0%; Score 2698; DB 4; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
DB 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

QY 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKFGKQVNEIGIYITDCMERAREVIPSQ 120  
DB 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKFGKQVNEIGIYITDCMERAREVIPSQ 120

QY 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFQGARITGOEAGYMI 180  
DB 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFQGARITGOEAGYMI 180

QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNQTIESPDNALQFR 240  
DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNQTIESPDNALQFR 240

QY 241 LYGDYNNVYTHSFLCYGKDQALWQKLAKDIOVASNEILRDPCHFPGYKKNVNSDLYKTP 300  
DB 241 LYGDYNNVYTHSFLCYGKDQALWQKLAKDIOVASNEILRDPCHFPGYKKNVNSDLYKTP 300

QY 301 CTKRFEMTLPPQOPEIIGIGNYQOCHQSILELFTSYCPYSQCAFNGIFLPPLOQDFGAF 360  
DB 301 CTKRFEMTLPPQOPEIIGIGNYQOCHQSILELFTSYCPYSQCAFNGIFLPPLOQDFGAF 360

QY 361 SAFYFVMKFLNLTSEKVSQEKVTENMKKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
DB 361 SAFYFVMKFLNLTSEKVSQEKVTENMKKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

QY 421 SLLLCGYHFTADSWEHIFIGIKIQSDAGWTGLYMLNTNMI PASQPLSTPLSHSTYVFL 480  
DB 421 SLLLCGYHFTADSWEHIFIGIKIQSDAGWTGLYMLNTNMI PASQPLSTPLSHSTYVFL 480

QY 481 MVLFSVLFTVAIIGLLIFHKPSYFWMKDV 510  
DB 481 MVLFSVLFTVAIIGLLIFHKPSYFWMKDV 510

RESULT 6

ADJ57262  
ID ADJ57262 standard; protein; 510 AA.  
AC ADJ57262;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human CD39 polypeptide.  
XX  
KW CD39; nucleoside diphosphate; thrombolytic; anticoagulant;  
KW cardiovascular; cytostatic; antibacterial; immunosuppressive; vasotropic;  
KW cardiant; antianginal; antiarteriosclerotic; gynaecological;  
KW cerebroprotective; cancer; human; apyrase; enzyme.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 55..61  
FT /note = ACR1  
FT Domain 125..135  
FT /note = ACR2  
FT Domain 171..183  
FT /note = ACR3  
FT Domain 213..220  
FT /note = ACR4  
FT Domain 447..454  
FT /note = ACR5  
XX  
FN WO2003070823-A2.  
XX

PD 28-AUG-2003.  
XX  
PF 19-FEB-2003; 2003WO-US004845.  
XX  
PR 20-FEB-2002; 2002US-0358303P.  
XX (GEO ) GEN HOSPITAL CORP.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Elmaleh DR, Robson SC, Papisov MI;  
XX  
DR MPI; 2003-778966/73.  
DR N-FSDB; ADJ57261.  
XX  
PT New enzyme polymer conjugate used for treating abnormal levels of  
PT extracellular nucleotides or platelet aggregation, graft transplant,  
PT cardiovascular disease, cancer and sepsis.  
XX  
PS Claim 20; SEQ ID NO 2; 82pp; English.  
XX  
CC The invention relates to a conjugate (I) comprising an enzyme and a  
CC biodegradable polymer, where (i) enzymatic activity of the enzyme is  
CC higher relative to that of the enzyme in the absence of the biodegradable  
CC polymer, or (ii) the half life of the enzyme is longer than that of the  
CC polymer in the absence of the polymer. The enzymatic activity (i) is at  
CC least 10 (preferably at least 100) times higher in the presence of the  
CC polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme,  
CC preferably an apyrase, especially a soluble form of CD39 and catalyzes  
CC hydrolysis of nucleoside diphosphate. The conjugate can be used to treat  
CC diseases relating to abnormal levels of extracellular nucleotides or  
CC abnormal aggregation of platelets, particularly cardiovascular disease,  
CC cancer, sepsis or a disease related to graft transplant. (I) is also used  
CC for treating coronary artery disease or injury following myocardial  
CC infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism,  
CC platelet associated ischaemic disorders including lung, coronary and  
CC cerebral ischaemia, reocclusion following thrombosis, thrombotic  
CC disorders, and thrombosis and coagulopathies associated with exposure to  
CC a foreign or injured tissue surface, in combination with angioplasty,  
CC carotid endarterectomy, anastomosis of vascular grafts and chronic  
CC cardiovascular devices. The present sequence represents a human CD39  
CC polypeptide.  
XX  
SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 7; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
DB 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

QY 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKFGKQVNEIGIYITDCMERAREVIPSQ 120  
DB 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKFGKQVNEIGIYITDCMERAREVIPSQ 120

QY 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFQGARITGOEAGYMI 180  
DB 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFQGARITGOEAGYMI 180

QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNQTIESPDNALQFR 240  
DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNQTIESPDNALQFR 240

QY 241 LYGDYNNVYTHSFLCYGKDQALWQKLAKDIOVASNEILRDPCHFPGYKKNVNSDLYKTP 300  
DB 241 LYGDYNNVYTHSFLCYGKDQALWQKLAKDIOVASNEILRDPCHFPGYKKNVNSDLYKTP 300

QY 301 CTKRFEMTLPPQOPEIIGIGNYQOCHQSILELFTSYCPYSQCAFNGIFLPPLOQDFGAF 360  
DB 301 CTKRFEMTLPPQOPEIIGIGNYQOCHQSILELFTSYCPYSQCAFNGIFLPPLOQDFGAF 360

QY 361 SAFYFVMKFLNLTSEKVSQEKVTENMKKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
DB 361 SAFYFVMKFLNLTSEKVSQEKVTENMKKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

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Db      361  |||||SAFYFWMKFLNLTSEKVSQEKVTEMKKFCAQFWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
QY      421  SLLQGYHFTADSWEHIFGKIQGS DAGWTLYMLNLTNMI PAEQPLSTPLSHSTYVFL 480
Db      421  SLLQGYHFTADSWEHIFGKIQGS DAGWTLYMLNLTNMI PAEQPLSTPLSHSTYVFL 480
QY      481  MVLFSLVLTFTVAIIGLLIFHKPSYFWKDMV 510
Db      481  MVLFSLVLTFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 7
ADL24295
ID   ADL24295 standard; protein; 510 AA.
XX
AC   ADL24295;
DT   03-JUN-2004 (first entry)
XX
DE   Human CD39.
XX
KW   cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30; OX40;
KW   antagonist.
XX
OS   Homo sapiens.
XX
PN   WO2004019866-A2.
XX
PD   11-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-US026354.
XX
PR   28-AUG-2002; 2002US-0406418P.
PR   12-AUG-2003; 2003US-0494457P.
XX
PA   (IMMUNEX ) IMMUNEX CORP.
XX
PI   Burton PB, Deisher TA;
XX
DR   WPI; 2004-239107/22.
DR   N-PSDB; ADL24294.
XX
PT   Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a
PT   cardiovascular disease, e.g. chronic immune myocarditis, congestive heart
PT   failure, aneurysm, angina, embolism, restenosis, ischemia or
PT   thrombocytopenic purpura.
XX
PS   Disclosure; Page 133-134; 135pp; English.
XX
CC   The present invention relates to a method of treating cardiovascular
CC   disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,
CC   CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40
CC   antagonists are useful for treating cardiovascular disorders, e.g.
CC   (chronic immune) myocarditis, congestive heart failure, aneurysms,
CC   angina, embolism, restenosis, ischemia or thrombocytopenic purpura. The
CC   present sequence is a polypeptide used in the exemplification of the
CC   invention.
XX
SQ   Sequence 510 AA;

```

```

Query Match      100.0%; Score 2698; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.2e-262;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  MEDTKESNVKTFCKNLAIFGSSIIAVALLAVGLTQNKALPENVKYGVILDGSSHT 60
Db      1  MEDTKESNVKTFCKNLAIFGSSIIAVALLAVGLTQNKALPENVKYGVILDGSSHT 60
QY      61  SLIYIKWPAEKENDTGTVVHQVEECRVKPGISKVFQKVNBEIGIYLTDCMERAREVIPRSQ 120
Db      61  SLIYIKWPAEKENDTGTVVHQVEECRVKPGISKVFQKVNBEIGIYLTDCMERAREVIPRSQ 120

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QY      121  HOETPVYLGATAGMRLLRMESEBELADRVLDVVVERSLSNYPDFQOGARIITGOEEGAYGWI 180
Db      121  HOETPVYLGATAGMRLLRMESEBELADRVLDVVVERSLSNYPDFQOGARIITGOEEGAYGWI 180
QY      181  TTYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNTQIESPDNALQPR 240
Db      181  TTYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNTQIESPDNALQPR 240
QY      241  LYKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASNEILRDPCHFPGYKKVNVSDLYKTP 300
Db      241  LYKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASNEILRDPCHFPGYKKVNVSDLYKTP 300
QY      301  CTKRFEMTLPFOQFBIQIGNYQQCHQSILELFTNTSYCPYSCAFNGIFLPLQGDGAF 360
Db      301  CTKRFEMTLPFOQFBIQIGNYQQCHQSILELFTNTSYCPYSCAFNGIFLPLQGDGAF 360
QY      361  SAFYFWMKFLNLTSEKVSQEKVTEMKKFCAQFWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db      361  SAFYFWMKFLNLTSEKVSQEKVTEMKKFCAQFWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
QY      421  SLLQGYHFTADSWEHIFGKIQGS DAGWTLYMLNLTNMI PAEQPLSTPLSHSTYVFL 480
Db      421  SLLQGYHFTADSWEHIFGKIQGS DAGWTLYMLNLTNMI PAEQPLSTPLSHSTYVFL 480
QY      481  MVLFSLVLTFTVAIIGLLIFHKPSYFWKDMV 510
Db      481  MVLFSLVLTFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 8
ADQ99453
ID   ADQ99453 standard; protein; 510 AA.
XX
AC   ADQ99453;
DT   23-SEP-2004 (first entry)
XX
DE   Human CD39 protein.
XX
KW   CD39-like protein; gene mapping; molecular weight marker;
KW   food supplement; anti-thrombotic; anti-tissue graft rejection agent;
KW   ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
KW   NTPase; human; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key Location/Qualifiers
FT   Region 47..68
FT   Region /note= "Apyrase region (ACR) I"
FT   Region 124..142
FT   Region /note= "Apyrase region (ACR) II"
FT   Region 169..191
FT   Region /note= "Apyrase region (ACR) III"
FT   Region 207..228
FT   Region /note= "Apyrase region (ACR) IV"
XX
PN   US6759214-B1.
XX
PD   06-JUL-2004.
XX
PF   13-JUL-2001; 2001US-00908510.
XX
PR   29-JAN-1999; 99US-00240639.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Chadwick BP, Frischauf A;
XX
DR   WPI; 2004-515395/49.
XX
PT   New CD-39-like polypeptides and polynucleotides, useful in chromosome and
PT   gene mapping, as molecular weight markers, as food supplements, or as
PT   anti-thrombotic or anti-tissue graft rejection agents.

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XX Example; Fig 8; 104pp; English.

XX The invention relates to novel CD39-like polypeptides (CD39-like nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding such polypeptides. CD39-like polynucleotides may be used as hybridisation probes, PCR primers and in chromosome and gene mapping. Polypeptides of the invention may be used as molecular weight markers, as food supplements, in generating an antibody that specifically binds the polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or for regulating ATP neurotransmission in smooth muscle, peripheral ganglia or brain. Sequences of the invention are useful in modulating ecto-ATPase activity and for identifying compounds that modulate ecto-ATPase activity. The present sequence is human CD39 protein, a member of the CD39-like protein family. Note: This sequence is stated to be the same as that shown as SEQ ID NO:13 in the sequence listing of the specification. However this sequence has additional residues at its ends.

XX Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510; Best Local Similarity 100.0%; Pred. No. 5.2e-262; Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVKTFCSKNIILAILGFSIIIVALLAVGLTQNKALPENVKYGVLDAGSSHT 60

Db 1 MEDTKESNVKTFCSKNIILAILGFSIIIVALLAVGLTQNKALPENVKYGVLDAGSSHT 60

Qy 61 SLIYIKVPAEKENDGVHVQVEECRVKGGISKFVKNEIGIYLTDCMERAREVIPSQ 120

Db 61 SLIYIKVPAEKENDGVHVQVEECRVKGGISKFVKNEIGIYLTDCMERAREVIPSQ 120

Qy 121 HQETPVYLGATAGMELLRMESEELADRLVDVVERSLSNYPDFQGARITGOEGAYGWI 180

Db 121 HQETPVYLGATAGMELLRMESEELADRLVDVVERSLSNYPDFQGARITGOEGAYGWI 180

Qy 181 TINYLKGFQSKTRWFSIVPVTNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 240

Db 181 TINYLKGFQSKTRWFSIVPVTNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 240

Qy 241 LYGDYNYVTHSFLCYGKDQALWOKLAKDIOVASNEILRDCPEHPGKVVNVDLYKTP 300

Db 241 LYGDYNYVTHSFLCYGKDQALWOKLAKDIOVASNEILRDCPEHPGKVVNVDLYKTP 300

Qy 301 CTKRFEMLTPQOPEIQIGNYQOCHQSIILFNSTSYCPYSQCAFNGIFLPPLOQDFGAF 360

Db 301 CTKRFEMLTPQOPEIQIGNYQOCHQSIILFNSTSYCPYSQCAFNGIFLPPLOQDFGAF 360

Qy 361 SAFYVVKFLNLTSEKVSQEKVTENMKKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTVIL 420

Db 361 SAFYVVKFLNLTSEKVSQEKVTENMKKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTVIL 420

Qy 421 SLLQGVHFTADSEHIFIGKIQSDAGWTLYGMLNLTNNIPAEQPLSTPLSHSTYVFL 480

Db 421 SLLQGVHFTADSEHIFIGKIQSDAGWTLYGMLNLTNNIPAEQPLSTPLSHSTYVFL 480

Qy 481 MVLFSVLFTVAITGLLIFHKPSPFWKDMV 510

Db 481 MVLFSVLFTVAITGLLIFHKPSPFWKDMV 510

RESULT 9

ADR69210

ID ADR69210 standard; protein; 510 AA.

XX

AC ADR69210;

XX

XX 04-NOV-2004 (first entry)

XX

XX Human CD39 protein #3.

XX

XX CD39-like protein; autoimmune deficiency disorder;

KW connective tissue disease; multiple sclerosis;

KW systemic lupus erythematosus; rheumatoid arthritis;

KW autoimmune pulmonary inflammation; Guillain-Barre syndrome;

KW autoimmune thyroiditis; insulin dependent diabetes mellitus;

KW myasthenia gravis; graft-versus-host disease;

KW autoimmune inflammatory eye disease; allergic disorder; asthma;

KW respiratory disorder; myeloid or lymphoid cell deficiency;

KW periodontal disease; tooth repair process; inflammatory bowel disease;

KW Crohn's disease; leukaemia; nervous system disorder; anticoagulant;

KW food supplement; anti-tissue graft rejection; ATP neurotransmission;

XX gene therapy; human.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

XX Region 47. .68

FT /note= "Apyrase region (ACR) I "

FT Region 124. .142

FT /note= "Apyrase region (ACR)II"

FT Region 169. .191

FT /note= "Apyrase region (ACR) III "

FT Region 207. .228

FT /note= "Apyrase region (ACR) IV"

XX

XX US6780410-B1.

XX 24-AUG-2004.

XX 13-JUL-2001; 2001US-00905744.

XX 29-JAN-1999; 99US-00240639.

XX (NUVE-) NUVELO INC.

XX Chadwick BP, Frischauf A;

XX WPI; 2004-613270/59.

XX

XX New isolated CD39LA polypeptide and polynucleotide, useful for preventing, treating, or ameliorating multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or graft-versus-host disease.

XX Example; Fig 8; 103pp; English.

XX

XX The present invention relates to CD39-like polypeptide and its encoding polynucleotide. The invention is useful for preventing, treating or ameliorating autoimmune deficiency disorders including connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease or autoimmune inflammatory eye disease, allergic disorders including asthma and other respiratory problems, myeloid or lymphoid cell deficiencies, periodontal diseases and other tooth repair processes, inflammatory conditions including inflammatory bowel disease and Crohn's disease, leukaemia and nervous system disorders. The invention is also useful as an anticoagulant for inhibiting platelet aggregation, food supplement, anti-tissue graft rejection agents, for regulating neurotransmission by ATP in smooth muscle, peripheral ganglia or brain and in gene therapy. The present sequence is a human CD39 protein. Note: This sequence is stated to be the same as that shown as SEQ ID 13 in sequence listing, however these sequences differ.

XX

XX Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510; Best Local Similarity 100.0%; Pred. No. 5.2e-262; Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVKTFCSKNIILAILGFSIIIVALLAVGLTQNKALPENVKYGVLDAGSSHT 60

Db 1 MEDTKESNVKTFCSKNIILAILGFSIIIVALLAVGLTQNKALPENVKYGVLDAGSSHT 60

QY	61	SLVIYKPAEKENDTGVVHVEECRVKPGISKFKVQVNEIGIYLTDCMERAREVLP	120
Db	61	SLVIYKPAEKENDTGVVHVEECRVKPGISKFKVQVNEIGIYLTDCMERAREVLP	120
QY	121	HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGI	180
Db	121	HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGI	180
QY	181	TINYLKGFQSKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNQTIESPDNALQ	240
Db	181	TINYLKGFQSKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNQTIESPDNALQ	240
QY	241	LYGKDVNVYTHSLFCYKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP	300
Db	241	LYGKDVNVYTHSLFCYKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP	300
QY	301	CTKRFEMTLPPQOFEIQIGNYQQCHQSILELFTNTSYCPYSQCAFNGIFLPLQGDGFA	360
Db	301	CTKRFEMTLPPQOFEIQIGNYQQCHQSILELFTNTSYCPYSQCAFNGIFLPLQGDGFA	360
QY	361	SAPYFVMKFLNLTSEKVSQEKVTEMKFKCAQPBWEIKTSYAGVKKYLSEYCFSGTYIL	420
Db	361	SAPYFVMKFLNLTSEKVSQEKVTEMKFKCAQPBWEIKTSYAGVKKYLSEYCFSGTYIL	420
QY	421	SLLLQGHYHTADSWEHIFIGIKIQGSDAGWTGLYMLNLNMIAPAOPLSTPLSHSYVFL	480
Db	421	SLLLQGHYHTADSWEHIFIGIKIQGSDAGWTGLYMLNLNMIAPAOPLSTPLSHSYVFL	480
QY	481	MVLSFLVLTVAIIGLLIFHKPSYFWKDMV	510
Db	481	MVLSFLVLTVAIIGLLIFHKPSYFWKDMV	510
RESULT 10			
ADRG9042			
ID	ADRG9042 standard; protein; 510 AA.		
AC	ADRG9042;		
XX	04-NOV-2004 (first entry)		
XX	Human CD39 protein #3.		
KW	CD39-like protein; CD39-like nucleotide triphosphatase; NTPase; cancer; leukaemia; acute lymphocytic leukaemia; acute myelocytic leukaemia; chronic leukaemia; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; Guillain-Barre syndrome; insulin dependent diabetes mellitus; myasthenia gravis; graft-versus-host disease; GVHD; allergic disorder; asthma; respiratory disorder; inflammatory disorder; septic shock; systemic inflammatory response syndrome; SIRS; Crohn's disease; central nervous system disorder; peripheral nervous system disorder; ischaemia; Parkinson's disease; Alzheimer's disease; Huntington's chorea; systemic lupus erythematosus; human immunodeficiency virus-associated myelopathy; transverse myelopathy; nutritional disorder; vitamin B12 deficiency; folic acid deficiency; Wernicke disease; tobacco-alcohol amblyopia; Marchiafava-Bignami disease; haemostatic activity; thrombolytic activity; nutritional supplement; ecto-ATPase activity; cytosolic; immunotherapy; human; enzyme.		
XX	Homo sapiens.		
Key	Location/Qualifiers		
FF	Region	47..68	
FT	Region	/note="Apyrase (ACR) I"	
FT	Region	124..142	
FT	Region	/note="Apyrase (ACR) II"	
FT	Region	169..191	
FT	Region	/note="Apyrase (ACR) III"	
FT	Region	202..228	
FT	Region	/note="Apyrase (ACR) IV"	
XX			
XX			

PN	US6780977-B1.		
XX			
PD	24-AUG-2004.		
XX			
PF	27-MAR-2002; 2002US-00107660.		
XX			
PR	29-JAN-1999; 99US-00240639.		
PR	13-JUL-2001; 2001US-00905589.		
XX	(NUVE-) NUVELO INC.		
PA			
XX			
PI	Chadwick BP, Frieschauf A;		
XX			
DR	WPI: 2004-613273/59.		
DR	GENBANK; S73813.		
XX			
PT	New antibody or its fragment that specifically binds to CD39L3 polypeptide, useful for detecting and purifying CD39L3 polypeptide, for treating leukemia, and for detecting and preventing metastatic spread of cancerous cells.		
PT	Example; Fig 8; 102pp; English.		
XX	The present invention provides novel CD39-like polypeptides (CD39-like nucleotide triphosphatase; NTPase) and their encoding polynucleotides. The invention is useful in treating cancer, leukaemia and related disorders such as acute lymphocytic leukaemia, acute myelocytic leukaemia and chronic leukaemia, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, Guillain-Barre syndrome, insulin dependent diabetes mellitus, myasthenia gravis and graft-versus-host disease, allergic disorders such as asthma, respiratory disorders, inflammatory disorders such as septic shock, systemic inflammatory response syndrome (SIRS) and Crohn's disease, central and peripheral nervous system disorders such as ischaemia, Parkinson's disease, Alzheimer's disease, Huntington's chorea, systemic lupus erythematosus, human immunodeficiency virus-associated myelopathy and transverse myelopathy and nutritional disorders such as vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia and Marchiafava-Bignami disease. The invention also has haemostatic and thrombolytic activity, serve as nutritional supplements and modulates ecto-ATPase activity. The invention acts as a cytostatic agent and is useful in immunotherapy. The present sequence is human CD39 protein. Note: This sequence is described in the specification as being the same as the human CD39 protein represented in SEQ ID NO: 13 of the sequence listing, however the two sequences are different.		
XX	Sequence 510 AA;		
QY	Query Match	100.0%; Score 2698; DB 8; Length 510;	
Db	Best Local Similarity	100.0%; Pred. No. 5.2e-262;	
QY	Matches 510; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 MEDTKESNVKTPCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGVILDGSSHT	60	
QY	1 MEDTKESNVKTPCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGVILDGSSHT	60	
Db	61 SLVIYKPAEKENDTGVVHVEECRVKPGISKFKVQVNEIGIYLTDGASGASTQVTFVPPQNGIITGOEAGYGI	120	
QY	61 SLVIYKPAEKENDTGVVHVEECRVKPGISKFKVQVNEIGIYLTDGASGASTQVTFVPPQNGIITGOEAGYGI	120	
Db	121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFDQFQARIITGOEAGYGI	180	
QY	121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFDQFQARIITGOEAGYGI	180	
Db	181 TINYLKGFQSKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNGIITGOEAGYGI	240	
QY	181 TINYLKGFQSKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNGIITGOEAGYGI	240	
Db	241 LYGKDVNVYTHSLFCYKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP	300	
QY	241 LYGKDVNVYTHSLFCYKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP	300	
Db	301 CTKRFEMTLPPFOQFETIGQIGNYQQCHQSILELFTNTSYCPYSQCAFNGIFLPLQGDGFGAF	360	
QY	301 CTKRFEMTLPPFOQFETIGQIGNYQQCHQSILELFTNTSYCPYSQCAFNGIFLPLQGDGFGAF	360	

Db 301 CTKRFEWTLPPQPFLOQIGNVQOCHQSILELNTSYCPYSQCAFNGIFLPLQDGFAG 360  
Qy 361 SAFYFVWKFLNLTSEKVSQEKVTEMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Db 361 SAFYFVWKFLNLTSEKVSQEKVTEMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Qy 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Qy 481 MVLFSLVLTVAIIIGLLIFHKPSYFWKDMV 510  
Db 481 MVLFSLVLTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 11  
ID ADS17924  
XX ADS17924 standard; protein; 510 AA.  
AC ADS17924;  
XX 18-NOV-2004 (first entry)  
DE Human CD39 protein #3.  
XX CD39-like protein; gene mapping; food supplement; ecto-ATPase activity;  
KW gene therapy; multiple sclerosis; rheumatoid arthritis;  
KW autoimmune thyroiditis; diabetes mellitus; myasthenia gravis;  
KW autoimmune inflammatory eye disease; osteoporosis; osteoarthritis;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW leukaemia; nervous system disorder; neuroprotective; antidiabetic;  
KW antirheumatic; antithyroid; immunosuppressive; antidiabetic;  
KW muscular-gen; ophthalmological; osteopathic; nootropic; antiparkinsonian;  
KW cystostatic; human; CD39 protein.  
XX Homo sapiens.

Key Location/Qualifiers  
FH Region 47..68  
FT /note= "Apyrase region (ACR) I"  
FT Region 124..142  
FT /note= "Apyrase region (ACR) II"  
FT Region 169..191  
FT /note= "Apyrase region (ACR) III"  
FT Region 207..228  
FT /note= "Apyrase region (ACR) IV"  
XX US6787328-B1.  
XX 07-SEP-2004.  
XX 13-JUL-2001; 2001US-00905732.  
XX 29-JAN-1999; 99US-00240639.  
XX (NUVE-) NUVELO INC.  
XX Chadwick BP, Frieschauf A;  
XX WPI; 2004-632929/61.  
XX New isolated CD39L4 polynucleotide, useful for preventing, treating, or  
XX ameliorating multiple sclerosis, rheumatoid arthritis, diabetes,  
XX osteoporosis, Alzheimer's disease, amyotrophic lateral sclerosis, or  
XX leukemia.  
XX Example; Fig 8; 103pp; English.

XX The present invention relates to a CD39-like polypeptides and the  
XX encoding polynucleotides. The CD39L4 polynucleotide is useful as  
XX hybridisation probes, as primers for PCR, for chromosome or gene mapping,  
XX in the recombinant production of protein, and in generation of antisense  
XX DNA or RNA. The protein of the invention is used as molecular weight

CC markers, and as food supplements and for modulating ecto-ATPase activity  
CC and for identifying compounds that can be utilised for modulating ecto-  
CC ATPase activity. The invention is useful for preventing, treating or  
CC ameliorating a medical condition, e.g. multiple sclerosis, rheumatoid  
CC arthritis, autoimmune thyroiditis, diabetes mellitus, myasthenia gravis,  
CC autoimmune inflammatory eye disease, osteoporosis, osteoarthritis,  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC leukaemia or nervous system disorders and in gene therapy. The present  
CC sequence is the human CD39 protein. Note: This sequence is stated to be  
CC the same as that shown as SEQ ID 13 in sequence listing, however these  
CC sequences differ.  
XX  
SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEDTKESNVKTFCSKNILAILGFFSIIIAVALLAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
Db 1 MEDTKESNVKTFCSKNILAILGFFSIIIAVALLAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
Qy 61 SLIYIKWPAEKENDTGVVHVEECRVKGGPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120  
Db 61 SLIYIKWPAEKENDTGVVHVEECRVKGGPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120  
Qy 121 HQETPVYLGATAGMRLLRMESEELADRLVDVVERSLSNYPDFQGARITTGQEGAYGI 180  
Db 121 HQETPVYLGATAGMRLLRMESEELADRLVDVVERSLSNYPDFQGARITTGQEGAYGI 180  
Qy 181 TINYLLGKFSQKTRWFSIVPVETNNQETFGALDLGGASTQVTFVQNTIESPDNALQPR 240  
Db 181 TINYLLGKFSQKTRWFSIVPVETNNQETFGALDLGGASTQVTFVQNTIESPDNALQPR 240  
Qy 241 LYGKDYNVYTHSFLCYGKQDALWQKLAKDIQVASNEILRDCPFHGYKKVNVSDLYKTP 300  
Db 241 LYGKDYNVYTHSFLCYGKQDALWQKLAKDIQVASNEILRDCPFHGYKKVNVSDLYKTP 300  
Qy 301 CTKRFEWTLPPQPFLOQIGNVQOCHQSILELNTSYCPYSQCAFNGIFLPLQDGFAG 360  
Db 301 CTKRFEWTLPPQPFLOQIGNVQOCHQSILELNTSYCPYSQCAFNGIFLPLQDGFAG 360  
Qy 361 SAFYFVWKFLNLTSEKVSQEKVTEMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Db 361 SAFYFVWKFLNLTSEKVSQEKVTEMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Qy 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Qy 481 MVLFSLVLTVAIIIGLLIFHKPSYFWKDMV 510  
Db 481 MVLFSLVLTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 12  
ABO84674  
ID ABO84674 standard; protein; 510 AA.  
XX ABO84674;  
AC ABO84674;  
XX 18-NOV-2004 (first entry)  
DT Human cancer-associated protein HP20-011.5.  
DE Human; cancer-associated protein; cytostatic; cancer; leukaemia;  
XX lymphoma; CAP.  
KW Homo sapiens.  
XX OS WO2004074320-A2.  
XX PN 02-SEP-2004.  
XX PD

XX 17-FEB-2004; 2004WO-US004730.  
 XX 14-FEB-2003; 2003US-00367094.  
 PR 14-MAR-2003; 2003US-00388838.  
 PR 15-APR-2003; 2003US-00417375.  
 PR 13-JUN-2003; 2003US-00461862.  
 PR 15-SEP-2003; 2003US-00663431.  
 PR 15-DEC-2003; 2003US-00737318.  
 XX (SAGR-) SAGRES DISCOVERY INC.  
 XX Morris DW, Morris DW, Malandro MS;  
 XX WPI; 2004-652914/63.  
 DR N-PSDB; ABD32958.  
 XX New isolated cancer-associated polynucleotides and polypeptides useful  
 PT for diagnosing, preventing or treating cancers, especially lymphoma and  
 PT leukemia, or in screening for agents that modulate cancer.  
 XX claim 18; seqid 698; 310pp; English.  
 XX The invention relates to an isolated nucleic acid comprising at least 10  
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given  
 CC in the specification, or its complement. The nucleic acids encode cancer-  
 CC associated proteins. Also included are an expression vector comprising  
 CC the isolated nucleic acid cited above, a host cell comprising the above  
 CC recombinant nucleic acid or expression vector, a microarray for detecting  
 CC a cancer-associated (CA) nucleic acid comprising at least one probe  
 CC comprising at least 10 contiguous nucleotides of any of the above-  
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within  
 CC an open reading frame of a CA sequence selected from any of the 95  
 CC polynucleotide sequences as mentioned in the specification, or its  
 CC complement), an isolated antibody, (or its antigen binding fragment) that  
 CC binds to the above polypeptide, a hybridoma that produces the above  
 CC monoclonal antibody, a pharmaceutical composition comprising the above  
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer  
 CC cells comprising the antibody cited above, methods for diagnosing cancer  
 CC or for detecting the presence or absence of cancer cells in an  
 CC individual, a method for inhibiting growth of cancer cells in an  
 CC individual, a method for delivering a therapeutic agent to cancer cells  
 CC in an individual, an electronic library comprising the above  
 CC polynucleotide or polypeptide (or their fragments), methods of screening  
 CC for anticancer activity or for a bioactive agent capable of modulating  
 CC the activity of a CA protein (CAP), methods for detecting cancer  
 CC associated with expression of a polypeptide in a test cell sample, a  
 CC method for treating cancers and a method for inhibiting the expression of  
 CC CA gene in a cell. The composition and methods are useful for detecting,  
 CC diagnosing, preventing and treating cancers, especially lymphoma and  
 CC leukaemia. These may also be used in screening for agents that modulate  
 CC cancer. The present sequence is a human CAP protein sequence. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 510 AA;  
 SQ

Query Match 100.0%; Score 2698; DB 8; Length 510;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
 Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEDTKESNVKTFCKNLAIGLGFSSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 60  
 DB 1 MEDTKESNVKTFCKNLAIGLGFSSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 60  
 QY 61 SLIYKWPASKENDTGVMVHVECRVKGPGISKFVQKVNEIGLYLTDCMERAREVIPSQ 120  
 DB 61 SLIYKWPASKENDTGVMVHVECRVKGPGISKFVQKVNEIGLYLTDCMERAREVIPSQ 120  
 QY 121 HQETPVYLGATAGWRLRMSESELADRVLDVRSLSNYPDFQGARITIQBEGAYGWI 180  
 DB 121 HQETPVYLGATAGWRLRMSESELADRVLDVRSLSNYPDFQGARITIQBEGAYGWI 180

QY 181 TINYLKGFSQKTRWFSIVPYETNNOETRGALDLGGASTQVTFVFPQNTIESPDNALQFR 240  
 DB 181 TINYLKGFSQKTRWFSIVPYETNNOETRGALDLGGASTQVTFVFPQNTIESPDNALQFR 240  
 QY 241 LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCHPGYKKVNVVSDLYKTP 300  
 DB 241 LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCHPGYKKVNVVSDLYKTP 300  
 QY 301 CTKRFEMTLFPOQFEIQQIGNYQQCHQSILELFTNTSYCPYSQCAFNGIFLPLQGGPFGAF 360  
 DB 301 CTKRFEMTLFPOQFEIQQIGNYQQCHQSILELFTNTSYCPYSQCAFNGIFLPLQGGPFGAF 360  
 QY 361 SAFYFVWKFLNLTSEKVSQEKVTEMKKFCAPWEIKTYSAGVKSEKYLSEYCFSGTYIL 420  
 DB 361 SAFYFVWKFLNLTSEKVSQEKVTEMKKFCAPWEIKTYSAGVKSEKYLSEYCFSGTYIL 420  
 QY 421 SLLQGYHFTADSWEHIFIGIKIQGSDAGWTLYGMLNLTNMIPTAEQPLSTPLSHSTYVFL 480  
 DB 421 SLLQGYHFTADSWEHIFIGIKIQGSDAGWTLYGMLNLTNMIPTAEQPLSTPLSHSTYVFL 480  
 QY 481 MVLFSLVLEFVAIIGLLIFHKPSYFWKDMV 510  
 DB 481 MVLFSLVLEFVAIIGLLIFHKPSYFWKDMV 510  
 RESULT 13  
 ADR87821  
 ID ADR87821 standard; protein; 510 AA.  
 XX ADR87821;  
 AC ADR87821;  
 DT 18-NOV-2004 (first entry)  
 XX Human CD39 protein #3.  
 DE Human CD39 protein #3.  
 XX CD39-like protein; CD39-like nucleotide-triphosphatase; NTPase;  
 KW HIV infection; hepatitis; multiple sclerosis;  
 KW systemic lupus erythematosus; rheumatoid arthritis;  
 KW Guillain-Barre syndrome; thyroiditis; diabetes; myasthenia gravis;  
 KW graft-versus-host disease; GHVD; asthma; human; human; enzyme; CD39.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 FH Key  
 FT Region 47..68 Location/Qualifiers  
 FT /note= "Apyrase region (ACR) I"  
 FT 125..142  
 FT /note= "Apyrase region (ACR) II"  
 FT 169..191  
 FT /note= "Apyrase region (ACR) III"  
 FT 207..228  
 FT /note= "Apyrase region (ACR) IV"  
 XX US6783959-B1.  
 PN 31-AUG-2004.  
 PD 27-MAR-2002; 2002US-00107576.  
 XX 29-JAN-1999; 99US-00240639.  
 PR 13-JUL-2001; 2001US-00908510.  
 XX (NUVE-) NUVELO INC.  
 PA Chadwick BP, Frischauf A;  
 PI WPI; 2004-623544/60.  
 XX GENBANK; S73813.  
 DR New isolated CD39/3 polypeptide and polynucleotide, useful for  
 PT diagnosing, preventing or treating HIV, hepatitis, multiple sclerosis,  
 PT systemic lupus erythematosus, arthritis, diabetes and asthma.

XX Example; Fig 8; 102pp; English.  
PS The invention relates to CD39-like polypeptides (CD39-like nucleotide-  
XX triphosphatase; NTPase) and their corresponding polynucleotides. The  
CC invention also relates to a method for making CD39L proteins. The methods  
CC and compositions of the invention are useful for the diagnosis,  
CC prevention and/or treatment of diseases or conditions associated with  
CC aberrant expression or activity of the CD39-like polypeptide, such as HIV  
CC infection, hepatitis, multiple sclerosis, systemic lupus erythematosus,  
CC rheumatoid arthritis, Guillain-Barre syndrome, thyroiditis, diabetes,  
CC myasthenia gravis, graft-versus-host disease (GVHD) and asthma. The  
CC present sequence is the human CD39 protein. Note: This sequence is  
CC described in the specification as being the same as the human CD39  
CC protein represented in SEQ ID NO: 13 of the sequence listing, however the  
CC two sequences are different.  
XX  
SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEDTKSNVKTFCCKNLAAILGFSIIIAVALLAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
DB 1 MEDTKSNVKTFCCKNLAAILGFSIIIAVALLAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
QY 61 SLIYKWPBAEKENDTGVVHVQVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120  
DB 61 SLIYKWPBAEKENDTGVVHVQVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120  
QY 121 HOETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARITQEGEGAYGWI 180  
DB 121 HOETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARITQEGEGAYGWI 180  
QY 181 TINYLKGFQSKTRWFSIVPYETNNQETFGALDGGASTQVTFVFNQTTIESPDNALQFR 240  
DB 181 TINYLKGFQSKTRWFSIVPYETNNQETFGALDGGASTQVTFVFNQTTIESPDNALQFR 240  
QY 241 LYGKDVNVYTHSFLCYGKDQALWQKLADIQVASNEILRDPCHFPGYKKVNVSDLYKTP 300  
DB 241 LYGKDVNVYTHSFLCYGKDQALWQKLADIQVASNEILRDPCHFPGYKKVNVSDLYKTP 300  
QY 301 CTKRFEMTLFQOPEIQIGNYQQCHQSIQLELNTSYCPYSCAFNGIFLPLQDGFAG 360  
DB 301 CTKRFEMTLFQOPEIQIGNYQQCHQSIQLELNTSYCPYSCAFNGIFLPLQDGFAG 360  
QY 361 SAFYPMKFLNLTSEKVSQEKVTEMMKFKCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420  
DB 361 SAFYPMKFLNLTSEKVSQEKVTEMMKFKCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420  
QY 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLNTNMPAEQPLSTPLSHSTYVFL 480  
DB 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLNTNMPAEQPLSTPLSHSTYVFL 480  
QY 481 MVLFSLVLTVAIIGLLIFHRPSYFWKDMV 510  
DB 481 MVLFSLVLTVAIIGLLIFHRPSYFWKDMV 510

RESULT 14  
ADK60421  
ID ADK60421 standard; protein; 511 AA.  
XX  
AC ADK60421;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Angiogenesis differentially expressed protein #61.  
KW vasotrophic; antirheumatic; antiarthritic; hypotensive; antianginal;  
KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;  
KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;

KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;  
KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;  
KW angioplasty; cicatrization; peripheral vascular disease; hypertension;  
KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;  
KW ischemia; angina; myocardial infarction; chronic heart disease;  
KW cardiac congestion; macular degeneration; osteoporosis.  
OS Homo sapiens.  
XX  
XX FR2836687-A1.  
PD 05-SEP-2003.  
XX  
PF 11-APR-2002; 2002FR-00004546.  
XX  
PR 04-MAR-2002; 2002FR-00002717.  
XX  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
XX  
XX Colin S, Schneider C, Al Mahmood S;  
XX  
XX WPI; 2004-013912/02.  
XX N-FSDB; ADK60414.  
XX  
XX Compositions for diagnosing, prognosing and treating angiogenic disorders  
XX including tumor vascularization and heart disease, comprise nucleic acid  
XX or polypeptide differentially expressed in angiogenesis.  
XX  
XX Claim 7; SEQ ID NO 297; 424pp; French.

The invention relates to a novel pharmaceutical composition active on  
angiogenesis comprising an endothelial cell nucleic acid whose expression  
is induced by an angiogenic factor and inhibited by an angiostatic agent  
or its complement or fragment, a polypeptide sequence encoded by the  
nucleic acid or its fragment, a molecule capable of inhibiting expression  
of the nucleic acid or a molecule which binds to the polypeptide  
sequence. The invention is used to diagnose, prognosis or treat an  
angiogenic disorder in a mammal, particularly a human. The disorder is  
particularly tumor vascularization, a retinopathy, rheumatoid arthritis,  
Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,  
endometriosis associated with neovascularization, restenosis due to  
angioplasty, overproduction of tissue due to cicatrization, a peripheral  
vascular disease, hypertension, vascular inflammation, Raynaud disease,  
aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,  
myocardial infarction, chronic heart disease, cardiac congestion or  
macular degeneration due to age or osteoporosis. This sequence  
corresponds to a protein encoded by a differentially expressed DNA used  
in the composition of the invention.

Sequence 511 AA;

Query Match 100.0%; Score 2698; DB 8; Length 511;  
Best Local Similarity 100.0%; Pred. No. 5.3e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKSNVKTFCCKNLAAILGFSIIIAVALLAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
DB 2 MEDTKSNVKTFCCKNLAAILGFSIIIAVALLAVGLTQNKALPENVKYGIIVLDAGSSHT 61  
QY 61 SLIYKWPBAEKENDTGVVHVQVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120  
DB 62 SLIYKWPBAEKENDTGVVHVQVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 121  
QY 121 HOETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARITQEGEGAYGWI 180  
DB 122 HOETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARITQEGEGAYGWI 181  
QY 181 TINYLKGFQSKTRWFSIVPYETNNQETFGALDGGASTQVTFVFNQTTIESPDNALQFR 240  
DB 182 TINYLKGFQSKTRWFSIVPYETNNQETFGALDGGASTQVTFVFNQTTIESPDNALQFR 241  
QY 241 LYGKDVNVYTHSFLCYGKDQALWQKLADIQVASNEILRDPCHFPGYKKVNVSDLYKTP 300



Db 242 LYCKDYNVYTHSFLCYGKQALAKQAKLADIQVANSNEILRDPCHFGYKVKVNVSDLYKTP 301  
Qy 301 CTKRFEMTLFPQOFETQIGNYQQCHQSILELNTSYCPYSQCAFNGIFLPPQLQDGFAG 360  
Db 302 CTKRFEMTLFPQOFETQIGNYQQCHQSILELNTSYCPYSQCAFNGIFLPPQLQDGFAG 361  
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKESYLSEYCFSGTYIL 420  
Db 362 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKESYLSEYCFSGTYIL 421  
Qy 421 SLLQGYHFTADSWEHIFGKIQGS DAGWTLGYMLNLTNMI PAEQPLSTPLSHSYVFL 480  
Db 422 SLLQGYHFTADSWEHIFGKIQGS DAGWTLGYMLNLTNMI PAEQPLSTPLSHSYVFL 481  
Qy 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510  
Db 482 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 511

RESULT 15  
ADK60722  
ID ADK60722 standard; protein; 511 AA.  
XX ADK60722;  
XX 06-MAY-2004 (first entry)  
XX Angiogenesis differentially expressed protein #61.  
XX vasotropic; anti-rheumatic; antiarthritic; hypotensive; anti-angiogenic;  
XX anti-inflammatory; cardiant; angiogenesis inhibitor; gene therapy;  
XX angiogenesis; endothelial cell; diagnosis; tumor vascularization;  
XX retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;  
XX ovary hyperstimulation; psoriasis; endometriosis; restenosis;  
XX angioplasty; cicatrization; peripheral vascular disease; hypertension;  
XX vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;  
XX ischemia; angina; myocardial infarction; chronic heart disease;  
XX cardiac congestion; macular degeneration; osteoporosis.  
XX Homo sapiens.  
XX FR2836686-A1.  
XX 05-SEP-2003.  
XX 04-MAR-2002; 2002FR-00002717.  
XX 04-MAR-2002; 2002FR-00002717.  
XX (GENE-) GENE SIGNAL.  
XX (ALMA/) AL MAHMOOD S.  
XX Colin S, Schneider C, Al Mahmood S;  
XX WPI; 2004-013911/02.  
XX N-PSDB; ADK60715.  
XX Compositions containing nucleic acid or polypeptide differentially  
XX expressed in angiogenesis are useful to diagnose, prognose and treat  
XX angiogenic disorders including tumor vascularization and heart disease.  
XX Claim 7; SEQ ID NO 297; 405pp; French.

XX The invention relates to a novel pharmaceutical composition active on  
XX angiogenesis comprising an endothelial cell nucleic acid whose expression  
XX is induced by an angiogenic factor and inhibited by an angiostatic agent  
XX or its complement or fragment, a polypeptide sequence encoded by the  
XX nucleic acid or its fragment, a molecule capable of inhibiting expression  
XX of the nucleic acid or a molecule which binds to the polypeptide  
XX sequence. The invention is used to diagnose, prognose or treat an  
XX angiogenic disorder in a mammal, particularly a human. The disorder is  
XX particularly tumor vascularization, a retinopathy, rheumatoid arthritis,

CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,  
CC endometriosis associated with neovascularization, restenosis due to  
CC angioplasty, overproduction of tissue due to cicatrization, a peripheral  
CC vascular disease, hypertension, vascular inflammation, Raynaud disease,  
CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,  
CC myocardial infarction, chronic heart disease, cardiac congestion or  
CC macular degeneration due to age or osteoporosis. This sequence  
CC corresponds to a protein encoded by a differentially expressed DNA used  
CC in the composition of the invention.  
XX SQ Sequence 511 AA;  
Query Match 100.0%; Score 2698; DB 8; Length 511;  
Best Local Similarity 100.0%; Pred. No. 5.3e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEDTKESNVKTFCSKNILAILGFSIIAVIALVGLTONKALPENVKYGVILDAGSSHT 60  
Db 2 MEDTKESNVKTFCSKNILAILGFSIIAVIALVGLTONKALPENVKYGVILDAGSSHT 61  
Qy 61 SLIYIKWPAEKENDTGVVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120  
Db 62 SLIYIKWPAEKENDTGVVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 121  
Qy 121 HQETPVYLGATAGMRLRMESEELADRVLDVVVERSLSNYPDFQGARIIITGOEEGAYGWI 180  
Db 122 HQETPVYLGATAGMRLRMESEELADRVLDVVVERSLSNYPDFQGARIIITGOEEGAYGWI 181  
Qy 181 TINYLLGKPSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPONQTIESP DNALQFR 240  
Db 182 TINYLLGKPSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPONQTIESP DNALQFR 241  
Qy 241 LYGKDYNVVTHSFLCYGKQDALWQKLAKDIOVANSNEILRDPCHFGYKVKVNVSDLYKTP 300  
Db 242 LYGKDYNVVTHSFLCYGKQDALWQKLAKDIOVANSNEILRDPCHFGYKVKVNVSDLYKTP 301  
Qy 301 CTKRFEMTLFPQOFETQIGNYQQCHQSILELNTSYCPYSQCAFNGIFLPPQLQDGFAG 360  
Db 302 CTKRFEMTLFPQOFETQIGNYQQCHQSILELNTSYCPYSQCAFNGIFLPPQLQDGFAG 361  
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKESYLSEYCFSGTYIL 420  
Db 362 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKESYLSEYCFSGTYIL 421  
Qy 421 SLLQGYHFTADSWEHIFGKIQGS DAGWTLGYMLNLTNMI PAEQPLSTPLSHSYVFL 480  
Db 422 SLLQGYHFTADSWEHIFGKIQGS DAGWTLGYMLNLTNMI PAEQPLSTPLSHSYVFL 481  
Qy 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510  
Db 482 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 511

Search completed: September 21, 2005, 16:19:46  
Job time : 92 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 21, 2005, 15:52:40 ; Search time 25 Seconds  
(without alignments)  
1962.822 Million cell updates/sec

Title: US-09-807-660C-2  
Perfect score: 2698  
Sequence: 1 MEDTKESNVKTFCSKNILAI.....VAIIIGLIIFHKPSYFWKDMV 510  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	100.0	510	2 I56242	lymphoid cell acti
2	511.5	19.0	483	2 D86276	hypothetical prote
3	469.5	17.4	405	2 E86276	hypothetical prote
4	455.5	16.9	630	2 S50463	hypothetical prote
5	435.5	16.1	572	2 T40856	probable nucleotid
6	421	15.6	516	2 G84442	probable nucleosid
7	413.5	15.3	485	2 T34147	hypothetical prote
8	402.5	14.9	508	2 C86276	7A19.33 protein -
9	397	14.7	557	2 T16696	hypothetical prote
10	381.5	14.1	556	2 T39109	probable guanosine
11	374.5	13.9	455	2 S48859	nucleoside triphos
12	352	13.0	1052	2 T04439	hypothetical prote
13	341.5	12.7	454	2 J04616	apyrase (BC 3.6.1
14	332	12.3	479	2 T23508	hypothetical prote
15	322.5	12.0	518	2 A40732	guanosine-diphosph
16	171	6.3	628	2 A55421	nucleoside-triphos
17	145.5	5.4	369	2 S77299	C4-dicarboxylase-b
18	122.5	4.5	727	2 T47541	beta-galactosidase
19	113	4.2	665	2 T18979	hypothetical prote
20	107.5	4.0	307	2 T27332	hypothetical prote
21	101.5	3.8	417	2 S53410	hypothetical prote
22	101.5	3.8	451	2 G59859	Mg2+ transporter h
23	101.5	3.8	716	2 T21516	hypothetical prote
24	101	3.7	1415	2 A72369	(R)-2-hydroxygluta
25	100	3.7	3848	2 T17414	TipC protein - sli
26	99	3.7	473	2 T15986	hypothetical prote
27	99	3.7	1951	2 B43963	RNA viral polymera
28	98.5	3.7	536	2 B90195	hypothetical prote
29	98.5	3.7	590	2 AB1411	autolysin, N-acety

RESULT 1

I56242  
lymphoid cell activation antigen - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I56242  
R:Maliszewski, C.R.; Delesepsee, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.;  
J. Immunol. 153, 3574-3583, 1994  
A:Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural char-  
A:Reference number: I56242; MUID:95015846; PMID:7930580  
A:Accession: I56242  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-510 <RES>  
A:Cross-references: UNIPROT:P49961; GB:S73813; NID:G765255; PIDN:AAB32152.1; PID:G765255  
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 100.0%; Score 2698; DB 2; Length 510;  
Best Local Similarity 100.0%; Pred. No. 4.1e-206;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEDTKESNVKTFCSKNILAILGFSIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHT	60
Db	1	MEDTKESNVKTFCSKNILAILGFSIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHT	60
Qy	61	SLYTYKWPAAEKENDTGVVHVQVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPRSQ	120
Db	61	SLYTYKWPAAEKENDTGVVHVQVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPRSQ	120
Qy	121	HOETPVYLGATAGMRLRMSEELADRLVDVVERSLSNYPDFQGARITGQEEGAYGWI	180
Db	121	HOETPVYLGATAGMRLRMSEELADRLVDVVERSLSNYPDFQGARITGQEEGAYGWI	180
Qy	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNQTIESPDNALQFR	240
Db	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNQTIESPDNALQFR	240
Qy	241	LYGKDYNYVTHSFICYGKDQALWQKLADIQVASNEILRDCPFHGYKKVNVVSLYKTP	300
Db	241	LYGKDYNYVTHSFICYGKDQALWQKLADIQVASNEILRDCPFHGYKKVNVVSLYKTP	300
Qy	301	CTKRFEMTLPPQFEIIOGIGNYQCHOSIILELFTNSYCPYSQCAFNGFLPLPQDQFAG	360
Db	301	CTKRFEMTLPPQFEIIOGIGNYQCHOSIILELFTNSYCPYSQCAFNGFLPLPQDQFAG	360
Qy	361	SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPMEEIKTSYAGVKEKYLSEYCSGTIYL	420
Db	361	SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPMEEIKTSYAGVKEKYLSEYCSGTIYL	420
Qy	421	SLLLQGHFTADSWEHIFGKIQSDAGWTLGYNLNTNMIPAEQPLSTPLSHSTYVFL	480
Db	421	SLLLQGHFTADSWEHIFGKIQSDAGWTLGYNLNTNMIPAEQPLSTPLSHSTYVFL	480

ALIGNMENTS



Query Match 16.9%; Score 455.5; DB 2; Length 630;  
Best Local Similarity 25.0%; Pred. No. 5.4e-28;  
Matches 139; Conservative 103; Mismatches 170; Indels 145; Gaps 25;

QY 46 NVKGVILDGSSHTSLIYKWP-----AEKENDTGV-----VHOVEECRVK-GPGI 91  
DB 7 NDRFGVIDAGSGSRILHVPKQDTESSLHATNQDSQILQSVPHIHOEKDWTFLNPLG 66

QY 92 SKFVQKNE-IGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEBELADRVLD 150  
DB 67 SFEKKPQDAYKSHIRPLDFAKNILPESHWSCPVFIQATAGWLL--PQDIQSSILD 123

QY 151 VVERSLNVPDFP-----QGARIITGOBEGAGVNTIYNLLGKFSOKTRWFSIVPYETN 204  
DB 124 GLCQGL-KHPAEFLVEDCSAQIQVIDGETELGYLGLNLYLGHFNYPN-----EVS 175

QY 205 NQETFGALDGGASTQVTFVPQNO-----TIESPDNALQFRLYGKDYNYTH 251  
DB 176 DHTFGMDGGASTQIAFAPHDSGEIARHDDIATIFLRSVNGDLQ-----KWDVFS 229

QY 252 SFLCYGKQOALMOKLADIQVA-----SNEILRDPCHFPGYKVVNVSDLYKT 299  
DB 230 TWLFGCANQARRRYLAQLINTLPENTNDYENDDFSTRNLNDPCMRG-----SSTDF--- 281

QY 300 PCKTREMFLPQOQFRIQIGIGNYQOCHQSILE-LFNYSYCPYSQCAFNGFIPLPQGD- 357  
DB 282 ----EPKDTI----FHIAAGSYEQCTKSIYPLLLKNMPCDDPCLFNGVHAPRI--DEA 331

QY 358 ----CAFSAFVPMKFLNLTSEKVSQEKVTEMMKFCQAPWEEI-----KTSYAGVKEK 407  
DB 332 NDKFICTSEYWTANDVFLKGBE-YNFDKPSLSREFCNSNMTQILANSKDGYSNIPEN 390

QY 408 YLSEYCFSGTYILSLLLQY----HFTADGWEHIH-----FTGKIQSDAGWTLGYML-- 456  
DB 391 FLKDACFKGNWVNLHLEGFDMPRIDVDA-ENVNDRPLFQSVKEKVEERELSWTLGRILLY 449

QY 457 -----NLTNMIPAE-----QPLSTPLSHSTYVFLMWLF 484  
DB 450 ASGSILAGNDDFMVGIAPSERRTKTKGKFIKGLLESQLRKQSSLSNKGFLMWFAII 509

QY 485 SLVFLFTVAIGLLIFHK 501  
DB 510 CCIFY-----LIFHR 519

RESULT 5  
T40856  
probable nucleoside triphosphatase - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T40856  
R:Ramppeiger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z21952  
A:Accession: T40856  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-572 <RAM>  
A:Cross-references: UNIPROT:Q9USP2; EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN00068; SPDB:  
A:Experimental source: strain 972h-; cosmid cille10  
C:Genetics:  
A:Gene: SPDB:SPCC11E10.05c  
A:Map position: 3

Query Match 16.1%; Score 435.5; DB 2; Length 572;  
Best Local Similarity 26.7%; Pred. No. 1.8e-26;  
Matches 144; Conservative 77; Mismatches 168; Indels 151; Gaps 22;

QY 48 KYGIVLDAGSSHTSLIYKWPAAKEN-----DTGVVHVQVEECRVKGPGRSKPV 95  
DB 4 KYGIFIDAGSSGRLLIYSWDYDTSLSKDKVKPLIETGTGIDGKWSLKVQPGISSFA 63

QY 96 QKVNEIG-IYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEBELADRVLDVVER 154

DB 64 NNPQHVKKHLKELLDDFAAAHPKDVHKETPVFLSATAGWRLIGVDAQ---NKLISHACR 120

QY 155 SL-SNYPDPF---QGARIITGOBEGAGVNTIYNLLGKFSOKTRWFSIVPYETNQETP 209

DB 121 YIKKNYDFDIPNCSNIRVIDKABGMYGWLATNYLLKTLBEK-----DTSTV 168

QY 210 GALDGGASTQVTF-VPONQTIESPD-----NALQFRLYGKDYNYVTHSFLCYGK 258

DB 169 GFLDGGASVQAFELPPSOLKNYKXDSISTVHIGLQNGOOL-----EYPLFVTTWLGFGA 223

QY 259 DOALMOKLAKOTQVASNEI---LRDPCFHPGKVVNVSDLYKTCTKRFEMTLPPQOPE 315

DB 224 NEAYRYLLGLLIESENGKVGNTLSDPCSLRG-----RTYDIDGIE 263

QY 316 IOGIGNYQOCHQSILELNTSY-CPYSQCAFNGFIPLPQGDGFGAFSAFVFMKFLNLTLS 374

DB 264 FAGTGDLKQCLKTYLNLNKKPCMDPCNFGISIPPV--DF-ANTFVGUSEFMYTTN 320

QY 375 EKVSQ-----EKVTEMMKFCQAPWEEI-----KTSYAGVKEKYLSEYCFSGTY 418

DB 321 DVFDMGGSYHFPNFYKVDK-----YCGTEWETMLSRLYNKELTPSTDENKLEKLCFKASW 376

QY 419 ILSLLLQ-----YHFTADGWEHIHFIKIQGSDAGWTLGYML 456

DB 377 ALNVLHEGFDVPKSNSTSSNDADKGLSVIPAYHSPFTSLE-----KIERTSVSWTLGQVL 430

QY 457 NLTN-----MIPAEQPLSTPLSH-----STYVFLMWVLSLVL 489

DB 431 LYASNOQLLAKPEYANYNDPYGKLIASPGKHMRLFPNKLFIISFIFCLFLFLSLVL 490

RESULT 6

G84442

probable nucleoside triphosphatase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C:Accession: G84442

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.;

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-516 <STO>

A:Cross-references: UNIPROT:O80612; GB:AE002093; NID:g3461821; PIDN:AAC32915.1; GSPDB:G6

C:Genetics:

A:Gene: At2g02970

A:Map position: 2

C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 15.6%; Score 421; DB 2; Length 516;

Best Local Similarity 26.5%; Pred. No. 2.2e-25;

Matches 136; Conservative 81; Mismatches 236; Indels 60; Gaps 15;



```
C;Genetics:
A;Gene: SPDB:SPAC824.08
A;Map position: 1

Query Match      14.1%; Score 381.5; DB 2; Length 556;
Best Local Similarity 27.1%; Pred. No. 3.4e-22;
Matches 121; Conservative 71; Mismatches 181; Indels 73; Gaps 17;

Qy    48 KYGIVLDAGSSHSYLYIKKPAKENDTGVVHQVEE--CRVKGRGISFKVOKNVEIGIYL 105
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    133 QYVLMTDAGSTGRVHYQP-----NNCNPSPKLEEFFFMIEPGLSFGADPEGAAASL 187

Qy    106 TDCMERAREVIPSQHQETPVYLGATAGMRLRMSEELADRVLDVVVERSLSN-YPPDPF- 163
       ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    188 DPLLDYAMENVPBEYRRCSPDIAVKATAG---LRLTGSEAKILKSVRQHLENDYPPIV 244
```

```

Db      243 KDVSVLEGSMEGIYAWITINYLGLTGKKA-----THSTVAVMDLGGASTQLV 293
Qy      223 FVPQ----NOTIESPNALQFRLYGKDYNVVYTHSFCLCYGKDOALWOKLANDIOVASNEIL 278
Db      294 FEFRPASDGSIVGDGHKYVDLYNGEQEYLIQHSLGYGLKEA--RKLHKFVLNNAEAL 351
Qy      279 RD-----PCFHFGYKKVNVNSDLYKTPTCKRFEM-----TLPFQQPFEIQIGI 320
Db      352 KESLELLGDSITSIIHPC LH-----LNASLTHPDSKSEASEVVFVGPSLAHLSLQCRGIA 405
Qy      321 NYOQC HQSILELNTSYCPYSQCAFNGIFLPPLOGDPG-----AFSAFYFMVKFLNLTSE 375
Db      406 E-----KALYKDKNCPRVPCSGFNHGHPKFETFTDSPYLVLIISFYDRMISLGMPSS- 456
Qy      376 KYSOEKVTMMKKFCAPQ--WEIEIKTSYAGVKE-KYLSEVCFSCTYTLSSLLOQYHFTAD 432
Db      457 TFTIEDMKYLANVCSGPTYWGDAFSLTDALKELKEPEWCMLDNLNYMSILLVSUGEYPNN 516
Qy      433 SWEIHIFIGKIQSDAGWTILGYMLNL 458
Db      517 --RQLHTAKKIDNKELGWCLGASLSM 540

RESULT 11
S48859
nucleoside triphosphatase precursor, chromatin-associated - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S65147; S48859
R:Heieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A>Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated,
A:Reference number: S65141; MUID:96157404; PMID:8616230
A:Accession: S65147
A:Molecule type: mRNA
A:Residues: 1-455 <RS2>
A:Cross-references: UNIPROT:P52914; EMBL:D32743; NID:g563611; PIDN:CAA03655.1;
C:Superfamily: nucleoside triphosphatase chromatin-associated
```

	Query Match	13.9%	Score 374.5	DB 2	Length 455
	Best Local Similarity	25.6%	Pred. No. 9.1e-22		
	Matches 120	Conservative 80	Mismatches 177	Indels 91	Gaps 19
Qy	37	LTQKAL---	PENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVH---	QVEECRVKGP	90
Db	29	LTSRKIFL	KOEELISSYAVFDAGTSGRIHVHF----	NONDLHLHGKVEYVYNNK	ITPG 84
Qy	91	ISKFGVKNEIGIYL	TDCMERAREVIPSROHQTTPVLTAGATAGMLRLMSEELADRVLD	150	
Db	85	LSYANNPQAAKSLI	PLLEEQADVDDLOQKTPVRLGNATGRLNLNGDASE---	KILQ	141
Qy	151	VVERSLN-YPDFQ--	GARIITQBEAGYGTITINYLLGKFSQKTRWFSGIVPYETNNQE	207	
Db	142	SYRDLMSNSTENVP	ADVAISIDTGOEGSYLWTVNVALCNLGKK-----	YTK	189

```
QY 208 TFGALDLGGASTQVTFVPQNOTIESPDNAL-----QFRLYKGDYNNVYTHSFLCYGKD 259
Db 190 TVGVIDLGGSVQMAVASKTAKNAKPVADGDDPKYIKKVLGKIYDLYVHSYILHFGR- 248
QY 260 QALWQKLAKDIQVASNEILR-----DPCPHPGYKKVNVNVDLYKTPCTKRFEMLTLPFOQ 313
Db 249 -----EASRAEILKLTSPSPNCLLAGFNGIITYSG-----EEFKAT----- 285
QY 314 FEIOGIGNYOCHOSILELNTSY-CPYSCAFNGIFLPPLOQDFG-----AFSAFYF 365
Db 286 -AVTSGANFNCKNTIRKALKNYPQCPYQNCCTFGGIW----NGGGNGQKNLPASSFFY 340
QY 366 VMKFLNLTSEK-----VSQKVTMMKKFCAQWEEIKTSYAGVKEKYLSEY-CFSGTYI 419
Db 341 LPEDTGMVDASTNFIPLRPVDIETKAECALAFEDAKSTYPLDKNQVASYVCMDLIIQ 400
QY 420 LSLLLQGYHFTADSWEHIFIGIQGSD-----AGWTILGYMLNTNMIP 463
Db 401 YVLLVDG--FGLDPLQKITSGKEIEYQDAIVEAANPLGNAVEAISALP 446

RESULT 12
T04439
hypothetical protein T18B16.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04439
R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Bancroft, I.; Mewes, H.W.
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15359
A:Accession: T04439
A:Molecule type: DNA
A:Residues: 1-1052 <BEV>
A:Cross-references: UNIPROT:O49676; EMBL:AL021687
A:Experimental source: cultivar Columbia; BAC clone T18B16
C:Genetics:
A:Map position: 4
A:Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A:Note: T18B16.150

Query Match 13.0%; Score 352; DB 2; Length 1052;
Best Local Similarity 26.5%; Pred. No. 1.9e-19;
Matches 114; Conservative 81; Mismatches 165; Indels 70; Gaps 18;

QY 89 PGISKFKVQKNEIGIYITDCMERAREVIPSQHOETPVYLGATGMRLLR-MESEBELADR 147
Db 578 PGFDKLVNRTGLKTAIKPLIOWAEKQIPKNAHRTTSLFYATAGVRRRLRPADSSWILGN 637
QY 148 VLDVVERSLNYPDP--QGARIITGOEEGAYGWITINY---LLGKFSOKTRWFSIVPYE 202
Db 638 VWSILAKS-----PFTCRREVWVKIISGTEEYFQGTALNYQTSMLGALPKKA----- 684
QY 203 TNNQETFGALDLGGASTQVTFVPQNOTIESPDNALQFRLYKGDYNNVYTHSFLCYGKDQA- 261
Db 685 -----TFGALDLGGSSLOVTF--ENEERTHETNLNLRIGSVNHLISAYSLAGYGLNDAF 737
QY 262 -----LWQKLA---KDIOVASNEILRDPCHFGPKYKKVNVNVDLYKTPCTKRFEMLTLPQ 312
Db 738 DRSVVHLKLLPNVKNSDLTIEGLEKMHKPCNLNSYN-----GVVICSQASSVQGGKKGK 792
QY 313 ---QFEIOGIGNYOCHOSILELNTSY-CPYSCAFNGIFLPPLOQDFGAFSAFYFMKF 369
Db 793 SGVSIKLVGAPNNGEC-----SALAKNAPCALPDGY-PRPHQGFYAVSGFFVYVYRF 842
QY 370 LNLTSKVQSEKVTMMKKFCAQWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHF 429
Db 843 FNLSAE-ASLDDVLEKREFCDKAWQARTSVS--PQPFIEQCFRAPYIVSLRLREGLYI 899
QY 430 TADSWEHIFIGIKQGSADGWTILGYMLNLTNMIPAEQPLSTPLSHSTYVPL-VWLFSLVL 488
Db 900 T----DKQIIIG---SGSITWTLGVAL-----LESKALSSLTGLKSYETLSMKINPIAL 947
```

```
QY 489 FTVAIIGLLI 498
Db 948 ISILILSLLL 957

RESULT 13
JC4616
apyrase (EC 3.6.1.5) precursor - potato
N:Alternate names: adenylpyrophosphatase; ATP-diphosphohydrolase
C:Species: Solanum tuberosum (potato)
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4616; PC4147
R:Handa, M.; Guidotti, G.
Biochem. Biophys. Res. Commun. 218, 916-923, 1996
A:Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from potato
A:Reference number: JC4616; MUID:96158985; PMID:8579614
A:Accession: JC4616
A:Molecule type: mRNA
A:Residues: 1-454 <HAN>
A:Cross-references: UNIPROT:P80595; GB:U58597; NID:GL381632; PIDN:AAB02720.1; PID:GL38163;
A:Accession: PC4147
A:Molecule type: protein
A:Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>
A:Experimental source: tubers
A:Note: The authors translated the codon GCA for residue 215 as Gly
C:Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydrolysis
of enzyme has nucleotide substrate specificity, divalent cation requirement, and insensitivity
olved in starch synthesis.
C:Genetics:
A:Gene: crop1
C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: glycoprotein; hydrolase; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:8-25/Domain: transmembrane #status predicted <TM>
F:31-454/Product: ATP-diphosphohydrolase #status predicted <MAT>
F:44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding
F:44-65/Region: nucleotide binding #status predicted
F:192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding
F:192-212/Region: nucleotide binding #status predicted
F:390-410,427-446/Region: hydrophobic carboxyl end
F:151,262/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 12.7%; Score 341.5; DB 2; Length 454;
Best Local Similarity 24.6%; Pred. No. 3.8e-19;
Matches 118; Conservative 85; Mismatches 193; Indels 83; Gaps 19;

QY 26 IIAVIALAVGLTQ---NKALP-----ENVKYGIVLDAGSSHTSLYIKWPAKEND 74
Db 12 ILAIFLVLPLSLSKNVNAQIPLRRHLLSHESEHYAVIFDAGTSGSRVHFRPD-EKLGL 70
QY 75 TGVHQQVECRVKGPGISKVFQKVNEIGIYITDCMERAREVIPSQHOETPVYLGATAGM 134
Db 71 LPIGNNIYFMATEPGLSSYAEADPKAAANSLEFLDGAEGVWPQELQSETPLDELGATAGL 130
QY 135 RLRLMESEBLADRVLDVVE---RSLSNYPDFQGARIITGOEEGAYGWITINYLLGKFSQ 191
Db 131 RMLKGA---AEKILQAVNLVKNQSTFHSKQWVITLDGTQEGSYMAAINVLLGNLGR 187
QY 192 KTRWFSIVPYETNNQSTFGALDLGGASTQVTFVPQN-QTIESPDN-----ALQFRLYK 244
Db 188 -----DYKSTTATIDLGGSVQMAVAISNEQFAKAPQNEDEGEPYVQQRHLMK 235
QY 245 DYNVYTHSFLCYGKDQALQKLAKDIQVASNEILRDPCHFGPKYKKVNVNVDLYKTPCTKR 304
Db 236 DYNLYVHSYILNGQ-LAGRAEIFKASRNSNPSCALEGC--DGYISYGGVD--YKWKAPKK 290
QY 305 FEMTLFPQFEIQIGNYOCHOSILELEN-TSYCPYSQCAFNGIFLPPLOQDFG----- 358
Db 291 G-----SSWKKCRLLTHALKINAKNIEECTFNQW---NGGGGQGN 332
QY 359 --AFSAFYFMKFLNLTSTSEKVSQE-----KVTEMMKKFCAQWEEIKTSYAGVKEKYLSE 411
Db 333 IHASSFFYDIGAQGVIVDTKFPFSALAKPIQYLNAKAVACQTNVADIKSIFPKPTQDRNIPY 392
```

```
Qy      412 YCPSGVYIISLLQLQGHHFTADSWEHIFHTGKIQSSD----AGWTLGYMLNL-----TNMI 462
Db      393 LCMDLIYEYTLVLDG--FGLNPHKEITVIHDVQYKNYLVGAAWPLGCALDLVSSTNNKI 449

RESULT 14
T23508
hypothetical protein K08H10.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23508
R/Gardner, A.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19750
A/Accession: T23508
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-479 <WIL>
A/Cross-references: UNIPROT:Q9XU84; EMBL:Z83113; PIDN:CAB05544.1; GSPDB:GN00020002
A/Experimental source: clone K08H10
C/Genetics:
A/Gene: CRSP:K08H10.4
A/Map position: 5
A/Introns: 36/3; 83/3; 189/1; 300/2; 412/3
C/Superfamily: nucleoside triphosphatase chromatin-associated
```

C>Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text\_change 09-Jul-2004

C/Accession: A40732; B40732; S30837; S50502  
R/Abeijon, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.B., J. Cell Biol. 122, 307-323, 1993

A>Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylation

A/Reference number: A40732; MUID:93308137; PMID:8391537

A/Accession: A40732

A/Molecule type: DNA

A/Residues: 1-518 <ABE>

A/Cross-references: UNIPROT:P32621; EMBL:L19560; NID:g349392; PIDN:AAA34656.1; PID:g349

A/Note: sequence extracted from NCBI backbone (NCBIN:134708, NCBIPI:134711)

A/Accession: B40732

A/Molecule type: protein

A/Residues: 125-144;238-257;276-281;366-374;399-412 <AB2>  
R/Mulligan, J.T.; Dietrich, F.S.; Hennessy, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993

A/Reference number: S30812

A/Accession: S30837

A/Molecule type: DNA

A/Residues: 1-518 <MUL>

A/Cross-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AAB65000.1; PID:g603637

R/Dietrich, F.S.  
submitted to the EMBL Data Library, December 1994

A>Description: The sequence of *S. cerevisiae* cosmids 8199, 8334, and 9871.

A/Reference number: S50491

A/Accession: S50502

A/Molecule type: DNA

A/Residues: 1-518 <DIE>

A/Cross-references: EMBL:U18779; NID:g603625; PIDN:AAB65000.1; PID:g603637; MIPS:YEL042

C/Genetics:

A/Gene: SGD:GDAL

A/Cross-references: SGD:S0000768; MIPS:YEL042W

A/Map position: 5L

C/Function:

A>Description: hydrolase

C/Superfamily: nucleoside triphosphatase chromatin-associated

C/Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein

F:10-24/Domain: transmembrane #status predicted <TMM>

F:41,280,/Binding site: carbohydrate (Asn) (covalent) #status predicted

DB 465 LSFQVLLHTGYDIPLQ--RELRTGKKIANKEIGWCLGASLPL 505

Search completed: September 21, 2005, 16:21:57  
Job time : 29 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 21, 2005, 13:13:33 ; Search time 91 Seconds  
(without alignments)  
2869.894 Million cell updates/sec

Title: US-09-807-660C-2  
Perfect score: 2698  
Sequence: 1 MDDTKSNVKTFCRKNILAI.....VAIIIGLLIHPKSPFWKDMV 510

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	100.0	510	1 ENP1_HUMAN	P49961 homo sapien
2	2096	77.7	510	1 ENP1_MOUSE	P55772 mus musculus
3	2091	77.5	510	2 Q921Q6	Q921Q6 mus musculus
4	2077	77.0	539	2 Q8CDV7	Q8CDV7 mus musculus
5	2057.5	76.3	511	1 ENP1_RAT	P97687 rattus norv
6	2006	74.4	510	1 ENP1_PIG	Q9MYU4 sus scrofa
7	1993	73.9	372	2 Q86VW3	Q86VW3 homo sapien
8	1982.5	73.5	513	1 ENP1_BOVIN	O18956 bos taurus
9	1693	62.8	420	2 Q8CEB1	Q8CEB1 mus musculus
10	1552	57.5	508	2 Q6DPS1	Q6DPS1 xenopus tro
11	1530	56.7	508	2 Q6GP74	Q6GP74 xenopus lae
12	1373.5	50.9	492	2 Q6DC46	Q6DC46 brachydanio
13	1063.5	39.4	497	2 Q6UQ22	Q6UQ22 mus musculus
14	1029.5	38.2	493	1 ENP1_CHICK	Q93295 gallus gall
15	1014.5	37.6	493	2 Q90X66	Q90X66 gallus gall
16	1004	37.2	495	1 ENP2_RAT	O35795 rattus norv
17	1001	37.1	495	1 ENP2_MOUSE	O55026 mus musculus
18	1001	37.1	495	2 Q921R1	Q921R1 mus musculus
19	982	36.4	454	2 Q6ZM69	Q6ZM69 brachydanio
20	981.5	36.4	494	1 ENP2_CHICK	P79784 gallus gall
21	981	36.4	526	2 Q6GN44	Q6GN44 xenopus lae
22	975	36.1	502	2 Q6L64	Q6L64 brachydanio
23	973.5	36.1	455	2 Q7T014	Q7T014 brachydanio
24	950	35.2	500	2 Q6NV19	Q6NV19 xenopus tro
25	942.5	34.9	529	1 ENP3_HUMAN	O75355 homo sapien
26	940	34.8	458	2 Q6UVZ0	Q6UVZ0 homo sapien
27	939.5	34.8	495	1 ENP2_HUMAN	Q9Y513 homo sapien
28	937.5	34.7	529	2 Q8OZ26	Q8OZ26 rattus norv
29	927	34.4	529	2 Q8BFW6	Q8BFW6 m mus muscu
30	860.5	31.9	453	2 Q6ZM68	Q6ZM68 brachydanio
31	843.5	31.3	452	2 Q8N6K2	Q8N6K2 homo sapien

32	698.5	25.9	544	2 Q7YTA4	Q7YTA4 schistosoma
33	629.5	23.3	300	2 Q8KOL2	Q8KOL2 mus musculus
34	596.5	22.1	209	2 Q8UVX9	Q8UVX9 torpedo mar
35	511.5	19.0	483	2 Q9XI62	Q9XI62 arabidopsis
36	510.5	19.0	488	2 Q6NQA8	Q6NQA8 arabidopsis
37	499	18.5	503	2 Q94AP8	Q94AP8 arabidopsis
38	499	18.5	503	2 Q8H1D8	Q8H1D8 arabidopsis
39	492	18.2	537	2 Q6Z543	Q6Z543 oryza sativ
40	490	18.2	336	2 Q8CCV2	Q8CCV2 mus musculus
41	488	18.1	634	2 Q6FRC2	Q6FRC2 candida gla
42	486	18.0	555	2 Q94E22	Q94E22 arabidopsis
43	482.5	17.9	611	2 Q6DH30	Q6DH30 brachydanio
44	480	17.8	555	2 Q8O612	Q8O612 arabidopsis
45	469.5	17.4	405	2 Q9M9T7	Q9M9T7 arabidopsis

#### ALIGNMENTS

RESULT 1  
ENP1\_HUMAN STANDARD; PRT; 510 AA.  
AC P49961; Q9UQ09; Q9Y3Q9;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)  
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell  
activation antigen) (Ecto-apyrase) (CD39 antigen).  
GN Name=ENTPDI; Synonym=CD39;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM VASCULAR).  
RX MEDLINE=95015846; PubMed=7930580;  
RA Maliszewski C.R., Dellespesse G.J.T., Schoenborn M.A., Armitage R.J.,  
RA Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,  
RA Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;  
RT "The CD39 lymphoid cell activation antigen. Molecular cloning and  
structural characterization.";  
RT J. Immunol. 153:3574-3583(1994).  
RL [2]  
RP SEQUENCE FROM N.A. (ISOFORM VASCULAR).  
RX TISSUE=Umbilical vein;  
RC MEDLINE=97149443; PubMed=8996251;  
RX Robson S.C., Kacmarek E., Siegel J.B., Candinas D., Koziak K.,  
RA Millan M., Hancock W.W., Bach F.H.;  
RT "Loss of ATP diphosphohydrolase activity with endothelial cell  
activation.";  
RL J. Exp. Med. 185:153-163(1997).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).  
RX TISSUE=Placenta;  
RC MEDLINE=93332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;  
RA Tateumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,  
RA Titani K., Fujimura Y., Narita N.;  
RT "The cDNA cloning of human placental ecto-ATP diphosphohydrolases I  
and II.";  
RT FEBS Lett. 453:335-340(1999).  
RL [4]  
RP SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.  
RC TISSUE=Placenta;  
RX MEDLINE=9609723; PubMed=8529670;  
RA Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;  
RT "Purification and properties of human placental ATP  
diphosphohydrolase.";  
RL Eur. J. Biochem. 234:66-74(1995).  
RN [5]  
RP SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND  
RP 399-405 (ISOFORM PLACENTAL I).  
RC TISSUE=Placenta;

RX MEDLINE=99062444; PubMed=9846014;  
RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,  
RA Sakamoto Y., Saito S., Ikeda S., Suzuki M., Titani K., Fujimura Y.,  
RT "Placental ecto-ATP diphosphohydrolase: its structural feature  
RT distinct from CD39, localization and inhibition on shear-induced  
RT platelet aggregation.";  
RL Int. J. Hematol. 68:297-310(1998).  
RN [6].  
RP FUNCTION.  
RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;  
RA Kaczmarek E., Koziak K., Seivigny J., Siegel J.B., Anrather J.,  
RA Beaudoin A.R., Bach F.H., Robson S.C.;  
RT "Identification and characterization of CD39/vascular ATP  
RT diphosphohydrolase.";  
RL J. Biol. Chem. 271:33116-33122(1996).  
RN [7].  
RP CHARACTERIZATION.  
RX MEDLINE=96215267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391;  
RA Wang T.F., Guidotti G.;  
RT "CD39 is an ecto-(Ca2+, Mg2+)-ATPase.";  
RL J. Biol. Chem. 271:9898-9901(1996).  
RN [8].  
RP PALMITOYLATION.  
RX MEDLINE=20102721; PubMed=10636909; DOI=10.1074/jbc.275.3.2057;  
RA Koziak K., Kaczmarek E., Kittel A., Seivigny J., Blusztajn J.K.,  
RA Schulte Am Esch J. II, Inai M., Guckelberger O., Goepfert C., Qawi I.,  
RA Robson S.C.;  
RT "Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to  
RT caveolae.";  
RL J. Biol. Chem. 275:2057-2062(2000).  
CC -I- FUNCTION: In the nervous system, could hydrolyze ATP and other  
CC nucleotides to regulate purinergic neurotransmission. Could also  
CC be implicated in the prevention of platelet aggregation.  
CC Hydrolyzes ATP and ADP equally well.  
CC -I- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.  
CC -I- COFACTOR: Requires calcium and magnesium.  
CC -I- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Names=Vascular;  
CC IsoId=P49961-1; Sequence=VSP\_003607;  
CC Names=Placental I;  
CC IsoId=P49961-2; Sequence=VSP\_003607;  
CC Names=Placental II;  
CC IsoId=P49961-3; Sequence=VSP\_003608, VSP\_003609,  
CC TISSUE SPECIFICITY: Expressed primarily on activated lymphoid  
CC cells. Also expressed in endothelial tissues. The vascular isoform  
CC and the placental isoform II are present in both placenta and  
CC umbilical vein, whereas placental isoform I is present in placenta  
CC only.  
CC -I- PTM: The N-terminus is blocked.  
CC -I- MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and  
CC 7.5-8.0 with ADP.  
CC -I- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.  
CC -I- DATABASE: NEMO=PROW; NOTE=CD guide CD39 entry; htm".  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd39.htm".  
-----  
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CC or send an email to license@isb-sib.ch).  
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DR EMBL: S73813; AAB32152.1; -;  
DR EMBL: U87967; AAB47572.1; -;  
DR EMBL: AJ133133; CAB41886.1; -;  
DR EMBL: AJ133134; CAB41887.1; -;  
DR PIR: I56242; I56242.  
DR Genbank: HGNC:3363; ENTPD1.  
DR MIM: 601752; -;

GO: GO:0005887; C: integral to plasma membrane; TAS.  
GO: GO:0007596; P: blood coagulation; TAS.  
InterPro: IPR000407; GDAL\_CD39\_NTPase.  
DR Pfam: PF01150; GDAL\_CD39; 1.  
DR PROSITE: PS01238; GDAL\_CD39\_NTPASE; 1.  
KW Alternative splicing; Antigen; Calcium; Direct protein sequencing;  
KW Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;  
KW Transmembrane.  
FT DOMAIN 1 16 Cytoplasmic (Potential).  
FT TRANSMEM 17 37 Potential.  
FT DOMAIN 38 478 Extracellular (Potential).  
FT TRANSMEM 479 499 Potential.  
FT DOMAIN 500 510 Cytoplasmic (Potential).  
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 457 457 N-linked (GlcNAc...) (Potential).  
FT VARSPLIC 1 4 MEDT -> MKGFKDLTSQQ (in isoform Placental  
FT I and isoform Placental II).  
FT VARSPLIC 272 299 /FTID=VSP\_003607.  
FT VARSPLIC 272 299 VASNEILRDPCHFGYKVKVNVSDLYKT -> ASITQSRPA  
FT PFTSAPPAPTSCCLFQIQ (in isoform Placental  
FT II).  
FT VARSPLIC 300 510 /FTID=VSP\_003608.  
FT Missing (in isoform Placental II).  
FT CONFLICT 57 58 SS -> G (in Ref. 5).  
FT CONFLICT 162 162 D -> K (in Ref. 4).  
FT CONFLICT 208 208 T -> TGET (in Ref. 5).  
FT CONFLICT 248 248 V -> Y (in Ref. 5).  
SQ SEQUENCE 510 AA; 57964 MW; BAD87D2499649159 CRC64;  
Query Match 100.0%; Score 2698; DB 1; Length 510;  
Best Local Similarity 100.0%; Pred. No. 1.5e-195;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEDTKESNVKTFCSKNILAILGFSIIAIVALLAVGLTQNKALPENVKYGVILDAGSSHT 60  
DB 1 MEDTKESNVKTFCSKNILAILGFSIIAIVALLAVGLTQNKALPENVKYGVILDAGSSHT 60  
QY 61 SLVIYKWPAAKENDTGTVHQQVEECRVKPGISKFKQVKNVEIGIYLTDCMERAREVIPSQ 120  
DB 61 SLVIYKWPAAKENDTGTVHQQVEECRVKPGISKFKQVKNVEIGIYLTDCMERAREVIPSQ 120  
QY 121 HQETPVYLGATAGMRLLRMESEBELADRVLDVVVERSLSNYPFDQFQARIITGOBEGAYGWI 180  
DB 121 HQETPVYLGATAGMRLLRMESEBELADRVLDVVVERSLSNYPFDQFQARIITGOBEGAYGWI 180  
QY 181 TINYLLGKFSOKTRWFESIYPYETNNQETFGALDLGGASTQVTFVPOQNTIESPDNALQFR 240  
DB 181 TINYLLGKFSOKTRWFESIYPYETNNQETFGALDLGGASTQVTFVPOQNTIESPDNALQFR 240  
QY 241 LYGKDVNVYTHSFLCYGKQDALWQKLAKDIQVANSNEILRDPCHFGYKVKVNVSDLYKTP 300  
DB 241 LYGKDVNVYTHSFLCYGKQDALWQKLAKDIQVANSNEILRDPCHFGYKVKVNVSDLYKTP 300  
QY 301 CTKRFEMLTPQOFEIQTGIGNYQQCHQSITLFTNTSYCPYSQCAFNGIFLPLPQGFAGF 360  
DB 301 CTKRFEMLTPQOFEIQTGIGNYQQCHQSITLFTNTSYCPYSQCAFNGIFLPLPQGFAGF 360  
QY 361 SAFYFVWKFLNLTSEKVSQEKVTENMKKCAQPWEEKTSYAGVKEKYLSEYCFSGTYIL 420  
DB 361 SAFYFVWKFLNLTSEKVSQEKVTENMKKCAQPWEEKTSYAGVKEKYLSEYCFSGTYIL 420  
QY 421 SLLLOQYHFTADSWEHIFIGIKIQGSDAGWTLGYMLNLNLMIPAEQPLSTPLSHSYVFL 480  
DB 421 SLLLOQYHFTADSWEHIFIGIKIQGSDAGWTLGYMLNLNLMIPAEQPLSTPLSHSYVFL 480  
QY 481 MYLFSLVLTVAIIGLLIFHKPSYFWKDWY 510  
DB 481 MYLFSLVLTVAIIGLLIFHKPSYFWKDWY 510

## RESULT 2

ENP1\_MOUSE STANDARD; PRT; 510 AA.

AC P55772; (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 44, Last annotation update)

DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)

DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).

GN Name=Entpdi; Synonym=Cd39;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95015846; PubMed=7930580;

RA Maliszewski C.R., Delespess G.J.T., Schoenborn M.A., Armitage R.J., Fangelow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K., Birke C., Albert D., Friend D., Gimpel S.D., Gayle R.B. III; "The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization.";

RT J. Immunol. 153:3574-3583(1994).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=129/SvJ;

RC MEDLINE=98199871; PubMed=9730622;

RX Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J., Gayle R.B. III, Maliszewski C.R.; "Gene structure and chromosome location of mouse Cd39 coding for an ecto-apyrase.";

RT Cytogenet. Cell Genet. 81:287-289(1998).

RL CC

CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other nucleosides to regulate purinergic neurotransmission. Could also be implicated in the prevention of platelet aggregation.

CC Hydrolyzes ATP and ADP equally well.

CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.

CC -!- COFACTOR: Requires calcium and magnesium (By similarity).

CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.

CC

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CC

DR EMBL; AF037366; AAC92259.1; -;

DR EMBL; AF041818; AAC83203.1; -;

DR EMBL; AF041812; AAC83203.1; JOINED.

DR EMBL; AF041813; AAC83203.1; JOINED.

DR EMBL; AF041814; AAC83203.1; JOINED.

DR EMBL; AF041815; AAC83203.1; JOINED.

DR EMBL; AF041816; AAC83203.1; JOINED.

DR EMBL; AF041817; AAC83203.1; JOINED.

DR MGD; MGI:102805; Entpdi.

DR GO; GO:0005605; C:basal lamina; IDA.

DR GO; GO:0004050; P:apyrase activity; IDA.

DR GO; GO:0006200; P:ATP catabolism; IDA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IDA.

DR GO; GO:00030168; P:platelet activation; IDA.

DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.

DR InterPro; IPR000407; GDA1\_CD39\_NTPase.

DR Pfam; PF01150; GDA1\_CD39\_1.

DR PROSITE; PS01238; GDA1\_CD39\_NTPASE; 1.

KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.

FT DOMAIN 1 16 Cytolaemic (Potential).

FT	TRANSMEM	17	37	Potential.
FT DOMAIN	38	478		Extracellular (Potential).
FT TRANSMEM	479	499		Potential.
FT DOMAIN	500	510		Cytolaemic (Potential).
FT CARBOHYD	73	73		N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	226	226		N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	291	291		N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	333	333		N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	428	428		N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	457	457		N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE	510 AA; 57205 MW; 86GA6113D2E13930 CRC64;			

Query Match 77.7%; Score 2096; DB 1; Length 510;

Best Local Similarity 76.0%; Pred. No. 5.4e-150;

Matches 389; Conservative 53; Mismatches 66; Indels 4; Gaps 3;

QY 1 MEDTRESNVKTFCSKNILAILGFSSIIAIVALLAVLQNKALPENVKYGVLDAGSSHT 60

DB 1 MEDIKSKVKRFSCKNLIILIGFTSILAVIALVGLTKNKLPEPVKVGIVLDAGSSHT 60

QY 61 SLIYKPAEKENDTGCVVHVQBECKVKGPGISKVQKVEIGIYLTDCMERAREVIPSQ 120

DB 61 NLIYKPAEKENDTGCVVQQLBECQVKGPGISKVYAKTDEIGAYLAECMELSTELPTSK 120

QY 121 HOETPVYLGATAGMRLMESEELADRLDVVERSLNYPDFQAGARIITGOEEGAYWI 180

DB 121 HHQTPVYLGATAGMRLMESESADEVLAAVSTSLKSYPPDFQGAKIITGOEEGAYWI 180

QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQNTQIESPDNALQPR 240

DB 181 TINYLLGRFTQEQSWLSLIS-DSQKQETFGALDGGASTQITFVQNSTIESPNSLQPR 239

QY 241 LYGDYNYVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVVNSLYKTP 300

DB 240 LYGEDYTYVYTHSFLCYGKQDQALWQKLAKDIOVSSGGVLKDCFCNFGYKVVVNSLYGTP 299

QY 301 CTKRFEMTLPPQFQFIQIGNYQQCHQSIILELNTSYCPYSCAFNGIPLPLQDGFAP 360

DB 300 CTKRFEKLLPFDQFRIQGTGQYEQCHQSIILELNNHSHCPYSCAFNGVLPPLHGSFGAP 359

QY 361 SAFYVPMKFLNLTSEK--VSQEKTEMKKCAQPMEEIKTSYAGVKEKYLSEYCFSGY 418

DB 360 SAFYVPMDFFKVAKNSVISQEKMTETIKNFCSKSWEETKTSYSPVKEKYLSEYCFSGAY 419

QY 419 ILSLLQGYHFTADSWEHIFGIQSGDAGWTLGYMLNLTNMIAPAEQPLSLPSSHSTYV 478

DB 420 ILS-LLQYNTDSSWEQIHFGKIKDSNAGWTLGYMLNLTNMIAPAEQPLSLPSSHSTYI 478

QY 479 FLMLVLSVLFTVAIIGLLIFHKPSYFWKDV 510

DB 479 GLMLVLSLLVAITGLFIYKPSYFWKEAV 510

## RESULT 3

Q921Q6 PRELIMINARY; PRT; 510 AA.

AC Q921Q6;

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Entpdi protein.

GN Name=Entpdi;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C25CH II; TISSUE=Mammary tumor;

EX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011278; AAH11278.1; -;  
DR MGD; MGI:102805; Entpdl.  
DR GO; GO:0005605; C:basal lamina; IDA.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0004050; F:aprase activity; IDA.  
DR GO; GO:0006200; P:ATP catabolism; IDA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IDA.  
DR GO; GO:0030168; P:platelet activation; IDA.  
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.  
DR Pfam; PF01150; GDAI CD39; 1.  
DR PROSITE; PS01238; GDAI CD39 NTPASE; 1.  
DR SEQUENCE 510 AA; 57176 MW; E77BB644AE1413A0 CRC64;  
SQ  
Query Match 77.5%; Score 2091; DB 2; Length 510;  
Best Local Similarity 75.8%; Pred. No. 1.3e-149;  
Matches 388; Conservative 53; Mismatches 67; Indels 4; Gaps 3;  
QY 1 MEDTKSNVKTFCCKNLAAILGFSIIAVIALAVALGTLQNKALPENVKYGVILDGSSHT 60  
DB 1 MEDIKDSKVKRCFKCNILILGFTSILAVIALAVGLTQNKLPENVKYGVILDGSSHT 60  
QY 61 SLYIYKPAEKENDTGTVHVECRVKGGISKFVKQVKNIEIGLYITDCHERAREVIPSQ 120  
DB 61 NLYIYKPAEKENDTGTVHVECRVKGGISKFVKQVKNIEIGLYITDCHERAREVIPSQ 120  
QY 121 HQETPVYLGATAGMRLRMESEBLADRVLDVVERLSNYPFDFOGARIITGOEGAYGWI 180  
DB 121 HQETPVYLGATAGMRLRMESEBLADRVLDVVERLSNYPFDFOGARIITGOEGAYGWI 180  
QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTPVQNTIESPDNALQPR 240  
DB 181 TINYLLGRTFTQESWLSLIS-DSQKQETFGALDGGASTQITVPQNSTIESPENSQPR 239  
QY 241 LYKQDYNVTHSPFLCYGKQALWQKLAKIOQVANSILRDCPHPGYKKVNVSDLYKTP 300  
DB 241 LYGEDYTVVTHSPFLCYGKQALWQKLAKIOQVANSILRDCPHPGYKKVNVSELYGTP 299  
QY 301 CTKRFEWTLPPFOQFEOIGNVOQCHQSILELPTNSVCPYSQCAFNGIFLPPQGFPGAP 360  
DB 300 CTRFERKKUPFDQFRLOGTGDEYQCHQSILELFNNSHCPYSQCAFNGVFLPPLHGSFGAP 359  
QY 361 SAFYFVYKFLNLTSEK--VSQEKVTBMKKFCAQPWEEIKTSYAGVKYLSYCFSGTY 418  
DB 360 SAFYFVMDFFPKVAKNSVISQERKWTETKTNFCSKSWEETKTSYPSVKYLSYCFSGAY 419  
QY 419 ILSLLQGYHTFADSEHWHIFIOKIGSDAGWTGLGMLNLTNMPAEQPLSTPLSHSTYV 478  
DB 420 ILS-LLQGYNFTDSSWEQHFHMGKIDSNAGWTGLGMLNLTNMPAEQPLSPPLSHSTYI 478  
QY 479 FLMLVLSVLFTVAITGLLIFHKPSPFWKDMV 510

DB 479 GLMVLFSLLLVAVAITGLFIYKSPSYFWKEAV 510  
RESULT 4  
Q8CDV7 PRELIMINARY; PRT; 539 AA.  
AC Q8CDV7;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
DE library, clone:4921511C05 product:ectonucleoside triphosphate  
DE diphosphohydrolase 1, full insert sequence.  
GN Name=Entpdl;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA The FANTOM Consortium;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,



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QY 1 MEDTKESNVKTCCKNLAAILGFSSTIAVALLAVGLTONKALPENVKYGVILDAAGSSHT 60
DB 1 MEDIKDSKVRKPCCKNLAAILGFSSTIAVALLAVGLTONKALPENVKYGVILDAAGSSHT 60
QY 61 SLVIYKWPAAEKENDTGVVHVEECRVKPGISKVFQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 NLYIYKWPAAEKENDTGVVHVEECRVKPGISKVFQKNEIGIYLTDCMERAREVIPSQ 120
QY 121 HOETPVYLGATAGMRLRLMESEBELADRLVDVVERSLSNYPFPDQGAARIITQGEAGYWI 180
DB 121 HOETPVYLGATAGMRLRLMESEBELADRLVDVVERSLSNYPFPDQGAARIITQGEAGYWI 180
QY 181 TYNILGKFSOKRWESIVPYETNNQETGALDLGGASTQVTPVPONOTIESPDNALQFR 240
DB 181 TYNILGKFSOKRWESIVPYETNNQETGALDLGGASTQVTPVPONOTIESPDNALQFR 240
QY 241 LYGKDYNNVYTHSFLCYGKQDQALWQKLAKDQIVASNEILRDPCCPHGPKYKVVVSDLYKTP 300
DB 241 LYGKDYNNVYTHSFLCYGKQDQALWQKLAKDQIVASNEILRDPCCPHGPKYKVVVSDLYKTP 300
QY 301 CTXKRFEMTLPPFOQFETQGIQGNVQOCHQSILELNTSCYPSQCAFNGIFLPPLOQDFGAF 360
DB 301 CTXKRFEMTLPPFOQFETQGIQGNVQOCHQSILELNTSCYPSQCAFNGIFLPPLOQDFGAF 360
QY 361 SAEFYFVMKEL-NLTSEKV-SOEKVTMMKKFCAQPEEIKTSYAGVKEKYLSEYCFSGTY 418
DB 361 SAEFYFVMKEL-NLTSEKV-SOEKVTMMKKFCAQPEEIKTSYAGVKEKYLSEYCFSGTY 418
QY 419 ILSLLQGVHFTADSEWHIFIGIKIQSGDAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTTV 478
DB 419 ILSLLQGVHFTADSEWHIFIGIKIQSGDAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTTV 478
QY 479 FLMLVLSVLFTVAITGLLIFHKPSYFWKDMV 510
DB 479 FLMLVLSVLFTVAITGLLIFHKPSYFWKDMV 510
QY 480 SLMLVLSVLVAMVITGLFIFSKPSYFWKEAV 511
DB 480 SLMLVLSVLVAMVITGLFIFSKPSYFWKEAV 511

RESULT 6
ENPL_PIG STANDARD; PRT; 510 AA.
AC QSMYU4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
DE Name=ENTPD1; Synonyms=CD39;
DE Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ortic endothelium;
RX MEDLINE=20325090; PubMed=10866813;
RA Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezak O.,
RA Seigney J.;
RA "Distribution, cloning, and characterization of porcine nucleoside
RT triphosphate diphosphohydrolase-1."
RL Eur. J. Biochem. 267:4106-4114(2000).
RN [2]
RP SEQUENCE OF 202-220.
RC TISSUE=Pancreas;
RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Koziak K., Seigney J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase."
RL J. Biol. Chem. 271:33116-33122(1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also

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CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Highest expression found in vascular
CC endothelium, smooth muscle, spleen and lung.
CC -!- PTM: Cleaved into two polypeptides that seem to stay together by
CC noncovalent interactions.
CC -!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.
CC
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CC
CC EMBL; AJ131746; CAB95871.1; -.
CC InterPro; IPR000407; GDAL_CD39_NTPase.
CC Pfam; PF01150; GDAL_CD39; 1.
CC PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
CC Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
CC Magnesium; Transmembrane.
CC CHAIN 1 510 Ectonucleoside triphosphate
CC dihydrophosphatase 1.
CC CHAIN 1 201 Ectonucleoside triphosphate
CC dihydrophosphatase 1 27 kDa subunit.
CC CHAIN 202 510 Ectonucleoside triphosphate
CC dihydrophosphatase 1 54 kDa subunit.
CC Cytoplasmic (Potential).
CC DOMAIN 1 16 Potential.
CC TRANSMEM 17 37 Extracellular (Potential).
CC DOMAIN 38 477 Potential.
CC TRANSMEM 478 498 Cytoplasmic (Potential).
CC DOMAIN 499 510 N-linked (GlcNAc. .) (Potential).
CC CARBOHYD 73 73 N-linked (GlcNAc. .) (Potential).
CC CARBOHYD 245 245 N-linked (GlcNAc. .) (Potential).
CC CARBOHYD 274 274 N-linked (GlcNAc. .) (Potential).
CC CARBOHYD 291 291 N-linked (GlcNAc. .) (Potential).
CC CARBOHYD 333 333 N-linked (GlcNAc. .) (Potential).
CC CARBOHYD 370 370 N-linked (GlcNAc. .) (Potential).
CC CARBOHYD 457 457 N-linked (GlcNAc. .) (Potential).
CC CONFLICT 203 203 G -> S (in Ref. 2).
CC SEQUENCE 510 AA; 57757 MW; 82F86869040D7735 CRC64;
CC
CC Query Match 74.4%; Score 2006; DB 1; Length 510;
CC Best Local Similarity 72.0%; Pred. No. 3.5e-143;
CC Matches 368; Conservative 69; Mismatches 72; Indels 2; Gaps 2;
QY 1 MEDTKESNVKTCCKNLAAILGFSSTIAVALLAVGLTONKALPENVKYGVILDAAGSSHT 60
DB 1 MEDRESEKLTFCCKNLAAILGFSSTIAVALLAVGLTONKALPENVKYGVILDAAGSSHT 60
QY 61 SLVIYKWPAAEKENDTGVVHVEECRVKPGISKVFQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 SLVIYKWPAAEKENDTGVVHVEECRVKPGISKVFQKNEIGIYLTDCMERAREVIPSQ 120
QY 121 HOETPVYLGATAGMRLRLMESEBELADRLVDVVERSLSNYPFPDQGAARIITQGEAGYWI 180
DB 121 HOETPVYLGATAGMRLRLMESEBELADRLVDVVERSLSNYPFPDQGAARIITQGEAGYWI 180
QY 181 TYNILGKFSOKRWESIVPYETNNQETGALDLGGASTQVTPVPONOTIESPDNALQFR 240
DB 181 TYNILGKFSOKRWESIVPYETNNQETGALDLGGASTQVTPVPONOTIESPDNALQFR 240
QY 241 LYGKDYNNVYTHSFLCYGKQDQALWQKLAKDQIVASNEILRDPCCPHGPKYKVVVSDLYKTP 300
DB 241 LYGKDYNNVYTHSFLCYGKQDQALWQKLAKDQIVASNEILRDPCCPHGPKYKVVVSDLYKTP 300
QY 301 CTXKRFEMTLPPFOQFETQGIQGNVQOCHQSILELNTSCYPSQCAFNGIFLPPLOQDFGAF 360
DB 301 CTXKRFEMTLPPFOQFETQGIQGNVQOCHQSILELNTSCYPSQCAFNGIFLPPLOQDFGAF 360

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Db 300 CTRRFLTSLPFPELEIQTGCTGDFOKCOQSIRPLFNTSYCPYSRCSFDCVFLPLPQGDFAAP 359
Qy 361 SAFYFVMKFLNLTSEKVS-QEKVTMMKKFCAQFWEEIKTSYAGVKEKYLSEYCFSGTYI 419
Db 360 SAFYFVMKFLNLTSEKVSFQSKVSTLEAFCSRPAELQWYFGDVKEKYLSEYCFSGTYI 419
Qy 420 LSLILQGYHFTADSWHEHIFIGIKQSDAGWTGLGYMLNTNMIPAPQPLSTPLSHSTYVF 479
Db 420 LTLILSGYHFTAEWTKNIHFMGKVQSTSVGWTGLGYMLNTNMIPSEPSSTRLSHSTYVF 479
Qy 480 LMVLFSLVLTVAIIIGLLIFHKPSYFWKDMV 510
Db 480 LMVLFSLVLTVAIIIGLLIFVCHRPYFWKDMV 510

RESULT 7
Q86VV3 PRELIMINARY; PRT; 372 AA.
AC Q86VV3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENTPD1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047664; AAH47664.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF0150; GDA1_CD39.1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 372 AA; 42731 MW; A8B1DE1366356EE3 CRC64;

Query Match 73.9%; Score 1993; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.3e-142; Gaps 0;
Matches 372; Conservative 0; Mismatches 0; Indels 0;

Qy 139 MESEELADRVLDVRSLSNYPDFQGARITIQEGEGAGWTITNYLLGKFSQKTRWFSI 198
Db 1 MESEELADRVLDVRSLSNYPDFQGARITIQEGEGAGWTITNYLLGKFSQKTRWFSI 60
Qy 199 VPEYTNNOETFGALDGGASTQVTVFQNTTIESPDNALQFLYXGKYNVYTHSFLCYGK 258
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Db 61 VPEYTNNOETFGALDGGASTQVTVFQNTTIESPDNALQFLYXGKYNVYTHSFLCYGK 120
Qy 259 DQALMQKLAKDQIVASNEILRDPCHPGYKVVVSDLYKTCTKRFEMTLFPQQFEIQG 318
|||||
Db 121 DQALMQKLAKDQIVASNEILRDPCHPGYKVVVSDLYKTCTKRFEMTLFPQQFEIQG 180
Qy 319 IGNYOQCHQSILLEFNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVS 378
Db 181 IGNYOQCHQSILLEFNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVS 240
Qy 379 QEKVTMMKKFCAQFWEEIKTSYAGVKEKYLSEYCFSGTYIILSLILQGYHFTADSWHEH 438
|||||
Db 241 QEKVTMMKKFCAQFWEEIKTSYAGVKEKYLSEYCFSGTYIILSLILQGYHFTADSWHEH 300
Qy 439 FIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFVLMVLFSLVLTVAIIIGLLI 498
|||||
Db 301 FIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFVLMVLFSLVLTVAIIIGLLI 360
Qy 499 FHKPSYFWKDMV 510
Db 361 FHKPSYFWKDMV 372

RESULT 8
ENPI_BOVIN
AC ENPI_BOVIN STANDARD; PRT; 513 AA.
ID O18956;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Econucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPdase) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (CD39 antigen) (Ecto-apyrase).
GN Name=ENTPD1; Synonyms=CD39;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RA Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RC TISSUE=Aorta;
RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase."
RL J. Biol. Chem. 271:33116-33122 (1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COPACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer, disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF005940; AAB62382.1; -
CC InterPro; IPR000407; GDA1_CD39_NTPase.
DR
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DR	Pfam: PF01150; GDAL CD39; 1.	
DR	PROSITE; PS01238; GDAL CD39_NTPASE; 1.	
KW	Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;	
KW	Magnesium; Transmembrane.	
FT	DOMAIN 1 16	Cytoplasmic (Potential).
FT	TRANSMEM 17 37	Potential.
FT	DOMAIN 38 481	Extracellular (Potential).
FT	TRANSMEM 482 502	Potential.
FT	DOMAIN 503 513	Cytoplasmic (Potential).
FT	CARBOHYD 73 73	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 227 227	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 245 245	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 307 307	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 336 336	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 373 373	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 460 460	N-linked (GLNAC. . .) (Potential).
FT	CONFLICT 97 97	K -> N (in Ref. 2).
FT	CONFLICT 101 103	INV -> CGF (in Ref. 2).
FT	CONFLICT 464 464	K -> V (in Ref. 2).
SQ	SEQUENCE 513 AA; 58113 MW; 20F598F27B6D2F96 CRC64;	
Query Match 73.5%; Score 1982.5; DB 1; Length 513;		
Best Local Similarity 70.8%; Pred. No. 2.1e-141;		
Matches 364; Conservative 73; Mismatches 72; Indels 5; Gaps 3;		
QY	1 MEDTKSNVTKFCNKILATLGFSSIIANTALAVGLTQNKALPENVKYGVILDGSSHT 60	
DB	1 MEDRESELKVFCSKILSLILGSCIIAVIALALGLTQNKALPENVKFGVILDGSSHT 60	
QY	61 SLVIYKPAEKENDTGVMHVECRVKPGISKFVQVNEIGLYLTDCMERAREVPRSQ 120	
DB	61 SLVIYKPAEKENDTGVMHVECRVKPGISKFVQVNEIGLYLTDCMERAREVPRSQ 120	
QY	121 HQETPVYLGATAGMRLRMESLADRLVDLVSRLSNYPDFQGAIRITQBEAGYWI 180	
DB	121 HMETPVYLGATAGMRLRMENKQADKILAAVASSISSEYPPDFQGAIRITQBEAGYWI 180	
QY	181 TYNILGKFSQKTRWFSIVPYETNNQETFGALDGLGASTQVTFVONQTIESPNDLQFR 240	
DB	181 TVNILLGKFTQKLSWFLNPKSKDDTQETYGALDGLGASTQITFVQNQETTESPNNLYFR 240	
QY	241 LYGDQNVYTHSLCYGKQDALQWKLAKOTQVANSNEILRDCPFHPGKVKVNVSDLYKTP 300	
DB	241 LYGNVSVYTHSLCYGKQDALQWKLAKOTQVANSNEILRDCPFHPGKVKVNVSDLYKTP 300	
QY	301 CTKRFEMT---LFPQGFQIIGNYQCHOSILELNTSYCPYSCAENGIFLPPLOQDF 357	
DB	300 CTKRHELNSSFYPLVDIEIRGAGNFQRCOSITQLENTSYCPYSSCSFNGVFLPLHGQF 359	
QY	358 GAFSAFYVMKFLNLTSEK-VSOEKVTEMKKCAQPWBEIKTSYAGVKEKYLSEYCFSG 416	
DB	360 GAFSAFYVMKFLNLTSEESVEQLTEKLEEFCAQRWEVEVQKNGFGEVKEKYLSEYCFSG 419	
QY	417 TYLSLLQGYHTFADSWEHIFGKIGSDAGWTGLCYMLNLTNMTPAEOPLSTPLSHST 476	
DB	420 TYLVLLNGYHTFADSWKNIHFWKVRSTVDGWTGLCYMLNLTNMTPAEPMSPPLPHST 479	
QY	477 YVFLMWLFSVLVFTVAIGLLIFHKPSYFWKDMV 510	
DB	480 YVFLMWLFSLLAVIIVGIWVFWKPSYFWKDMV 513	
RESULT 9		
Q8CEB1		
ID	PRELIMINARY; PRT; 420 AA.	
AC	Q8CEB1	
DT	01-MAR-2003 (TrEMBLrel. 23, Created)	
DT	01-MAR-2003 (TrEMBLrel. 25, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched	
DE	library, clone:4732419M16 product:ectonucleoside triphosphate	
GN	diphosphohydrolase 1, full insert sequence. (Fragment).	
GN	Name=Entp1;	

OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	
RX	Carinci P., Hayashizaki Y.;	
RA	"High-efficiency full-length cDNA cloning.";	
RL	Meth. Enzymol. 303:19-44 (1999).	
RN	[2]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;	
RX	RIKEN FANTOM Consortium;	
RA	"Functional annotation of a full-length mouse cDNA collection.";	
RL	Nature 409:685-690 (2001).	
RN	[3]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	The FANTOM Consortium;	
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;	
RL	"Analysis of the mouse transcriptome based on functional annotation of	
RT	60,770 full-length cDNAs.";	
RL	Nature 420:563-573 (2002).	
RN	[4]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;	
RX	Carinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,	
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;	
RL	"Normalization and subtraction of cap-trapper-selected cDNAs to	
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";	
RL	Genome Res. 10:1617-1630 (2000).	
RN	[5]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;	
RX	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,	
RA	Konno H., Akiyama J., Nishi K., Kitsumi T., Tashiro H., Itoh M.,	
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,	
RA	Fujimoto R., Matsumoto H., Sakaguchi S., Ikegami T., Watahiki M.,	
RA	Yamawake S., Inoue K., Togawa Y., Izawa K., Ohara E., Watahiki M.,	
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,	
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;	
RT	"RIKEN integrated sequence analysis (RISA) system-384-Format	
RT	sequencing pipeline with 384 multicapillary sequencer.";	
RL	Genome Res. 10:1757-1771 (2000).	
RN	[6]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,	
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,	
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,	
RA	Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,	
RA	Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,	
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,	
RA	Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,	
RA	Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,	
RA	Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,	
RA	Tagawa A., Takahashi F., Takaku-Akai H., Tanaka Y., Tanaka T.,	
RA	Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;	
RL	Submitted (JULY-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AK028625; BAC26037.1; -.	
DR	MGD; MGI:102805; Entp1.	
DR	GO; GO:005605; C:basal lamina; IDA.	
DR	GO; GO:0016021; C:integral to membrane; TAS.	
DR	GO; GO:0004050; F:ATPase activity; IDA.	
DR	GO; GO:0006780; P:ATP catabolism; IDA.	
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IDA.	
DR	GO; GO:0030168; P:platelet activation; IDA.	
DR	GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.	



DR InterPro: IPR000407; GDAI\_CD39\_NTPase.  
DR Pfam: PF01150; GDAI\_CD39; 1.  
DR PROSITE: PS01238; GDAI\_CD39\_NTPASE; 1.  
FT Hydrolase.  
KW NON TER  
SQ SEQUENCE 1 1 420 AA; 47261 MW; 1369E747CD4B9CE7 CRC64;  
  
Query Match 62.8%; Score 1693; DB 2; Length 420;  
Best Local Similarity 73.9%; Pred. No. 1.3e-119;  
Matches 312; Conservative 46; Mismatches 60; Indels 4; Gaps 3;  
  
QY 91 ISKFKVKNVEIGYLTDCMERAREVTPRSQHOETPVYLGATAGMRLRMSESELADRVLD 150  
DB 1 ISKYAKTDEIGAYLAECMELSTELPTSKGHQTPVYLGATAGMRLRMSESQSADEVLA 60  
  
QY 151 VVERSLSNYPFDQAGARIITQBEAGAYGMITNLLGKFSQKTRWPSIVPYETNNQETFG 210  
DB 61 AVSTLSKSPYFPDQAGAKIITQBEAGAYGMITNLLGRTQBSWLSLIS-DSQKETFG 119  
  
QY 211 ALDGGASTQVTPVQNTIESPDNALQRLYKGVNVTYTHSFLCYGKQDALWQKLAKDI 270  
DB 120 ALDGGASTQITVPQNTIESPNSLQRLYGEDYTVYTHSFLCYGKQDALWQKLAKDI 179  
  
QY 271 OVASNEILRDCPHFGYKVVNVSDLYKTPCTKREPMITLPFOQFEIQQGNYQCHQSIL 330  
DB 180 QVSSGGVLKDCPNPGYKVVNVSDLYKTPCTKREPKLPFOQFRIQGTGDEYQCHQSIL 239  
  
QY 331 ELFNYSYCPYSCAFNGIFLPLQDGFAGFSAFYFVWKFLNLTSEK--VSQSKVTMMKK 388  
DB 240 ELFNNSHCYSCAFNGVFLPLHGSFGAFSAFYFVMDFFKVAKNVSISQSKMTITKN 299  
  
QY 389 FCAQPMEEIKTSYAGYKYLSEYCFSGTYIISLLQGYHFTADSWEHIHFQIKIGSDA 448  
DB 300 FCSKSWETKTSYPSVKEKYLSEYCFSGAYILS-LLQGYNFTGSSWEQIHFGKIKDSNA 358  
  
QY 449 GWTGLYMLNTNMIPAEQPLTPLSHTYVFLMWLFSVLFVTAIGLILFHKPSYFWKD 508  
DB 359 GWTGLYMLNTNMIPAEQPLTPHSTYIGLWVLSLLVAITGLPIYKPSYFWKE 418  
  
QY 509 MV 510  
DB 419 AV 420  
  
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AC Q6DFS1  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Entpd1-prov protein.  
GN Name=entpd1-prov;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8364;  
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RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Mair M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Gerhard D.S.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC076662; AAH76662.1; -  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR InterPro; IPR000407; GDAI\_CD39\_NTPase.  
DR Pfam; PF01150; GDAI\_CD39; 1.  
DR PROSITE; PS01238; GDAI\_CD39\_NTPASE; 1.  
SQ SEQUENCE 508 AA; 57322 MW; 12CAEAC05BEABDEB CRC64;  
  
Query Match 57.5%; Score 1552; DB 2; Length 508;  
Best Local Similarity 55.9%; Pred. No. 7.9e-109;  
Matches 285; Conservative 92; Mismatches 131; Indels 2; Gaps 2;  
  
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QY 61 SLIYKPAEKENDTGVVHQVEECVKVQKSGKFKVQKNEIGIYLTDCMERAREVTPRSQ 120  
DB 61 SVYIYEWPAEKENDTGVVQVQINECKVEGNISSYGHEPLKAGLSLQCKNKAQVPEKQ 120  
  
QY 121 HOETPVYLGATAGMRLRMSESELADRVLDVVERSLSNYPFDQAGARIITQBEAGAYGI 180  
DB 121 QRETPVYLGATAGMRLRMSESELADRVLDVVERSLSNYPFDQAGARIITQBEAGAYGI 180  
  
QY 181 TINVLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQNTIESPDNALQPR 240  
DB 181 TINVLGNGFIQDSGWFKYIP-NFKPTETSGALDGGASTQITFESKRE-IESQENSLHFR 238  
  
QY 241 LYGDKNVYTHSFLCYGKQDALWQKLAKDIQVANSNEILRDCPHFGYKVVNVSDLYKTP 300  
DB 239 LYGKSYDIYTHSFLCYGKQDALWQKLAKDIQVANSNEILRDCPHFGYKVVNVSDLYKTP 298  
  
QY 301 CTKRFEWTLPEQFEIQQGNYQCHQSILENTSYCPYSCAFNGIFLPLQDGFAGF 360  
DB 299 CISKLRPTAPSTLDIRGTGNYQCKRNQVQIFNRTHCTYSHCSFNGVFPQSLDGTFFGAF 358  
  
QY 361 SAFYFVWKFLNLTSEKVSQKVTMMKKFCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
DB 359 SAYYFVNMFLNLTNEQMSLDKVKETVERHCSRDPWDEVKDKPKIKEKYLSEYCFSGTYIL 418  
  
QY 421 SLLQGYHFTADSWEHIHFQIKIGSDAGWTLGYMLNLTNMIPAEQPLTPLSHTYVFL 480  
DB 419 NLLEYGYGFSSENWDIRFLGKIDSDAGWTLGYMLNLTNMIPAEQPLTPLSHTYVFL 478  
  
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AC Q6GP74  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE MG80631 protein.  
GN Name=MG80631;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;







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Job time : 94 secs

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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:03:34 ; Search time 28 Seconds  
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Title: US-09-807-660C-2  
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Scoring table: BLOSUM62  
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	100.0	510	3	US-08-930-921-1
2	2698	100.0	510	4	US-09-781-796C-1
3	2650	98.2	502	4	US-09-557-800C-55
4	2650	98.2	502	4	US-09-370-625A-38
5	1171.5	43.4	282	4	US-09-949-016-7977
6	942.5	34.9	529	3	US-09-240-639-4
7	942.5	34.9	529	4	US-09-908-510A-4
8	942.5	34.9	529	4	US-09-905-744B-4
9	942.5	34.9	529	4	US-10-107-660-4
10	942.5	34.9	529	4	US-10-107-576-4
11	942.5	34.9	529	4	US-09-905-732B-4
12	942.5	34.9	529	4	US-09-923-304-4
13	942.5	34.9	529	4	US-09-949-016-6049
14	942.5	34.9	529	4	US-09-905-743B-4
15	938.5	34.8	556	4	US-09-949-016-11328
16	897	33.2	479	4	US-09-949-016-11559
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37	442.5	16.4	153	4	US-09-905-743B-15	Sequence 15, Appl
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39	427	15.8	462	4	US-09-123-112-2	Sequence 2, Appl
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41	417.5	15.5	150	3	US-09-240-639-16	Sequence 16, Appl
42	417.5	15.5	150	4	US-09-908-510A-16	Sequence 16, Appl
43	417.5	15.5	150	4	US-09-905-744B-16	Sequence 16, Appl
44	417.5	15.5	150	4	US-10-107-660-16	Sequence 16, Appl
45	417.5	15.5	150	4	US-10-107-576-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-930-921-1  
; Sequence 1, Application US/08930921B  
; Patent No. 6287837  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; APPLICANT: SEVIGNY, Jean  
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN  
; CURRENT APPLICATION NUMBER: US/08/930,921B  
; CURRENT FILING DATE: 1998-01-02  
; EARLIER APPLICATION NUMBER: PCT/CA96/00223  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 510  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: unknown  
US-08-930-921-1

Query Match	100.0%	Score 2698;	DB 3;	Length 510;
Best Local Similarity	100.0%	Pred. No. 5.8e-277;		
Matches 510;	Conservative	0;	Mismatches	0;
			Indels	0;
Gaps				0;
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Db 361 SAFYFVMKFLNLTSEKVSQEKVTEMKKKCAQPWBEIKTYSYAGVKSEKYLSEYCFSGTYIL 420  
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Db 421 SLLQGYHFTADSWEHIFGKIQGSADAGWTGLGYMLNLTNMIIPAEQPLSTPLSHSYVFL 480  
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RESULT 2  
US-09-781-796C-1  
; Sequence 1: Application US/09781796C  
; Patent No. 6800284  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; APPLICANT: SEVIGNY, Jean  
; APPLICANT: BACH, Fritz H.  
; APPLICANT: ROBSON, Simon  
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: 920333.90019  
; CURRENT APPLICATION NUMBER: US/09/781.796C  
; PRIOR FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 08/419,204  
; PRIOR FILING DATE: 1995-04-10  
; PRIOR APPLICATION NUMBER: CA96/00223  
; PRIOR FILING DATE: 1996-04-10  
; PRIOR APPLICATION NUMBER: 08/930,921  
; PRIOR FILING DATE: 1998-02-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 510  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-781-796C-1

Query Match 100.0%; Score 2698; DB 4; Length 510;  
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; Sequence 55, Application US/09557800C  
; Patent No. 6476211  
; GENERAL INFORMATION:  
; APPLICANT: Mulero, John  
; APPLICANT: Ford, John  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 28110/36457  
; CURRENT APPLICATION NUMBER: US/09/557,800C  
; CURRENT FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/122449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/244444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-557-800C-55

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 16:21:29 ; Search time 521 Seconds  
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398.419 Million cell updates/sec

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Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2698	100.0	510	10 US-09-781-796B-1	Sequence 30, Appl
4	2698	100.0	510	16 US-10-646-308-30	Sequence 2, Appli
5	2698	100.0	511	18 US-10-922-378-2	Sequence 297, App
6	2698	100.0	511	18 US-10-934-998-297	Sequence 97, Appl
7	2677	99.2	517	18 US-10-934-998-97	Sequence 38, Appl
8	2650	98.2	502	13 US-10-092-063-38	Sequence 27, Appl
9	2358	87.4	464	9 US-09-835-147-27	Sequence 2, Appli
10	2348	87.0	439	9 US-09-374-586-2	Sequence 6, Appli
11	2348	87.0	454	9 US-09-835-147-6	

12	2348	87.0	463	9 US-09-835-147-30	Sequence 30, Appl
13	2348	87.0	473	9 US-09-835-147-29	Sequence 29, Appl
14	2348	87.0	474	9 US-09-835-147-28	Sequence 28, Appl
15	2348	87.0	476	9 US-09-835-147-3	Sequence 3, Appli
16	2348	87.0	478	9 US-09-835-147-8	Sequence 8, Appli
17	2348	87.0	487	9 US-09-835-147-26	Sequence 26, Appl
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ALIGNMENTS

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; Sequence 2, Application US/09835147  
; Patent No. US20020002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 510  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-835-147-2

Query Match 100.0%; Score 2698; DB 9; Length 510;  
Best Local Similarity 100.0%; Pred. No. 1.3e-233;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374, 586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
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; ORGANISM: HOMO-SAPIEN
US-09-374-586-1
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; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
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Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US2004013692A1  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, Paul B. J.  
; APPLICANT: DEISHER, Theresa A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE  
; FILE REFERENCE: 3432-B  
; CURRENT APPLICATION NUMBER: US/10/646,308  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: --to be assigned--  
; PRIOR FILING DATE: 2003-08-12  
; PRIOR APPLICATION NUMBER: 60/406,418  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 30  
; LENGTH: 510  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-646-308-30  
Query Match 100.0%; Score 2698; DB 16; Length 510;  
Best Local Similarity 100.0%; Pred. No. 1.3e-233;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
Db 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
Qy 61 SLIYIKWPAEKENDTGVVHVQVEECRVKPGISKFGKVEIGIYLTDCMERAREVIPSQ 120  
Db 61 SLIYIKWPAEKENDTGVVHVQVEECRVKPGISKFGKVEIGIYLTDCMERAREVIPSQ 120  
Qy 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQCARITGOEGAYGWI 180  
Db 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQCARITGOEGAYGWI 180  
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 240  
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 240  
Qy 241 LYGDYNYVTHSLCYGKQDQALWQKLAKDIOVASNEILRDCPFHPGYKKVNVNSLYKTP 300  
Db 241 LYGDYNYVTHSLCYGKQDQALWQKLAKDIOVASNEILRDCPFHPGYKKVNVNSLYKTP 300  
Qy 301 CTKRFEMLTPFOQFEIQGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPPLOQDFGAF 360  
Db 301 CTKRFEMLTPFOQFEIQGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPPLOQDFGAF 360  
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEIKTSYAGVKEKYLSEYCFSGTYIL 420

Db 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Qy 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Qy 481 MVLFSLVLTFTVAIIGLLIFHKPSYFWKDMV 510  
Db 481 MVLFSLVLTFTVAIIGLLIFHKPSYFWKDMV 510  
RESULT 5  
US-10-922-378-2  
; Sequence 2, Application US/10922378  
; Publication No. US2005016998A1  
; GENERAL INFORMATION:  
; APPLICANT: ELMALEH, DAVID R.  
; APPLICANT: ROBSON, SIMON C.  
; APPLICANT: PAPISOV, MIKHAIL L.  
; TITLE OF INVENTION: CONJUGATES COMPRISING A BIODEGRADABLE POLYMER AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: ELA-004.01  
; CURRENT APPLICATION NUMBER: US/10/922,378  
; CURRENT FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: PCT/US03/04845  
; PRIOR FILING DATE: 2003-02-19  
; PRIOR APPLICATION NUMBER: 60/358,303  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin ver. 3.3  
; SEQ ID NO 2  
; LENGTH: 510  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-922-378-2  
Query Match 100.0%; Score 2698; DB 18; Length 510;  
Best Local Similarity 100.0%; Pred. No. 1.3e-233;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
Db 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
Qy 61 SLIYIKWPAEKENDTGVVHVQVEECRVKPGISKFGKVEIGIYLTDCMERAREVIPSQ 120  
Db 61 SLIYIKWPAEKENDTGVVHVQVEECRVKPGISKFGKVEIGIYLTDCMERAREVIPSQ 120  
Qy 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQCARITGOEGAYGWI 180  
Db 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQCARITGOEGAYGWI 180  
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 240  
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 240  
Qy 241 LYGDYNYVTHSLCYGKQDQALWQKLAKDIOVASNEILRDCPFHPGYKKVNVNSLYKTP 300  
Db 241 LYGDYNYVTHSLCYGKQDQALWQKLAKDIOVASNEILRDCPFHPGYKKVNVNSLYKTP 300  
Qy 301 CTKRFEMLTPFOQFEIQGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPPLOQDFGAF 360  
Db 301 CTKRFEMLTPFOQFEIQGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPPLOQDFGAF 360  
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Db 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Qy 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Qy 481 MVLFSLVLTFTVAIIGLLIFHKPSYFWKDMV 510

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Db 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
|||||
RESULT 6
US-10-934-998-297
; Sequence 297, Application US/10934998
; Publication No. US20050153917A1
; GENERAL INFORMATION:
; APPLICANT: AL-MAHMOOD, SALMAN
; APPLICANT: COLIN, SYLVIE
; APPLICANT: SCHNEIDER, CHRISTOPHE
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
; FILE REFERENCE: BMA-04-1206
; CURRENT APPLICATION NUMBER: US/10/934, 998
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/FR03/00695
; PRIOR FILING DATE: 2003-03-04
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 297
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CDS protein of the sequence Genbank/S73813 (seq ID 290)
US-10-934-998-297

Query Match 100.0%; Score 2698; DB 18; Length 511;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVILVDAGSSHT 60
Db 2 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVILVDAGSSHT 61
61 SLVIYKWPAAKENDTGTVVHVQVEECRVKPGISKVFQKVNEIGIYLTDCMERAREVIPSQ 120
Db 62 SLVIYKWPAAKENDTGTVVHVQVEECRVKPGISKVFQKVNEIGIYLTDCMERAREVIPSQ 121
121 HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWI 180
Db 122 HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWI 181
181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPOQTIESPDNALQPR 240
Db 182 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPOQTIESPDNALQPR 241
241 LYGKDYNVYTHSFLCYGKQOALWQKLAKOIQVASNEILRDPCHPGYKVVVSDLYKTP 300
Db 242 LYGKDYNVYTHSFLCYGKQOALWQKLAKOIQVASNEILRDPCHPGYKVVVSDLYKTP 301
301 CTKRFEMTLFPQOFIEIGIGNYQOCHQSIIELENTSYCPYSQCAFNGIFLPPLOGDFGAF 360
Db 302 CTKRFEMTLFPQOFIEIGIGNYQOCHQSIIELENTSYCPYSQCAFNGIFLPPLOGDFGAF 361
361 SAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKESYSEYCFSGTYIL 420
Db 362 SAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKESYSEYCFSGTYIL 421
421 SLLLGQVHTADSWEHIFHTGKIQGS DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 480
Db 422 SLLLGQVHTADSWEHIFHTGKIQGS DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 481
481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
Db 482 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 511

RESULT 7
US-10-934-998-97
; Sequence 97, Application US/10934998
; Publication No. US20050153917A1
; GENERAL INFORMATION:
; APPLICANT: AL-MAHMOOD, SALMAN
; APPLICANT: COLIN, SYLVIE
; APPLICANT: SCHNEIDER, CHRISTOPHE
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
; FILE REFERENCE: BMA-04-1206
; CURRENT APPLICATION NUMBER: US/10/934, 998
; CURRENT FILING DATE: 2004-09-03
; PRIOR FILING DATE: 2003-03-04
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CDS protein of the sequence GS-N45: 184..1737 (GS-P45)
US-10-934-998-97

Query Match 99.2%; Score 2677; DB 18; Length 517;
Best Local Similarity 100.0%; Pred. No. 1e-231;
Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVILVDAGSSHTSLVI 64
Db 12 KESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVILVDAGSSHTSLVI 71
65 YKWPAAKENDTGTVVHVQVEECRVKPGISKVFQKVNEIGIYLTDCMERAREVIPSQHOET 124
Db 72 YKWPAAKENDTGTVVHVQVEECRVKPGISKVFQKVNEIGIYLTDCMERAREVIPSQHOET 131
125 PVLGATAGMRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWTITNY 184
Db 132 PVLGATAGMRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWTITNY 191
185 LLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPOQTIESPDNALQPRLYGK 244
Db 192 LLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPOQTIESPDNALQPRLYGK 251
245 DYNVYTHSFLCYGKQOALWQKLAKOIQVASNEILRDPCHPGYKVVVSDLYKTPCTKR 304
Db 252 DYNVYTHSFLCYGKQOALWQKLAKOIQVASNEILRDPCHPGYKVVVSDLYKTPCTKR 311
305 FEMTLFPQOFIEIGIGNYQOCHQSIIELENTSYCPYSQCAFNGIFLPPLOGDFGAFSAFY 364
Db 312 FEMTLFPQOFIEIGIGNYQOCHQSIIELENTSYCPYSQCAFNGIFLPPLOGDFGAFSAFY 371
365 FVWKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKESYSEYCFSGTYILSLL 424
Db 372 FVWKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKESYSEYCFSGTYILSLL 431
425 QGYHFTADSWEHIFHTGKIQGS DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSTYVFLMVL 484
Db 432 QGYHFTADSWEHIFHTGKIQGS DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSTYVFLMVL 491
485 SLVLFVTVAIIIGLLIFHKPSYFWKDMV 510
Db 492 SLVLFVTVAIIIGLLIFHKPSYFWKDMV 517

RESULT 8
US-10-092-063-38
```

; Sequence 38, Application US/10092063  
; Publication No. US20020173005A1  
; GENERAL INFORMATION:  
; APPLICANT: Mulero, John  
; APPLICANT: Mulero, Julio  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES  
; FILE REFERENCE: 28110/35908  
; CURRENT APPLICATION NUMBER: US/10/092,063  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350,836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273,447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/244,444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/122,449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-092-063-38

Query Match 98.2%; Score 2650; DB 13; Length 502;  
Best Local Similarity 100.0%; Pred. No. 2.7e-229;  
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEDTKEVNKTCCKNIIAILGFSIIIVALLAVGLTQNKALPENVKYIGVLDAGSSHT	60
DB	1	MEDTKEVNKTCCKNIIAILGFSIIIVALLAVGLTQNKALPENVKYIGVLDAGSSHT	60
QY	61	SLYIVKPAEKNDGTGVHVEECRVKPGISKFQKNEIGIYLTDCMERAREVIPRSQ	120
DB	61	SLYIVKPAEKNDGTGVHVEECRVKPGISKFQKNEIGIYLTDCMERAREVIPRSQ	120
QY	121	HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGQEGAYGWI	180
DB	121	HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGQEGAYGWI	180
QY	181	TINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQPR	240
DB	181	TINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQPR	240
QY	241	LYGKDVNVYTHSFLCYGKQDQALWOKLAKDIOVASNEILRDPCHFPGYKVVNSDLYKTP	300
DB	241	LYGKDVNVYTHSFLCYGKQDQALWOKLAKDIOVASNEILRDPCHFPGYKVVNSDLYKTP	300
QY	301	CTKREMTLPFOQFEIQIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPLQDGFCAF	360
DB	301	CTKREMTLPFOQFEIQIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPLQDGFCAF	360
QY	361	SAFYFMKFLNLTSEKVSQEKYTEMMKKFCAQWPBEIKTSYAGVKEKYLSEYCFSGTVIL	420
DB	361	SAFYFMKFLNLTSEKVSQEKYTEMMKKFCAQWPBEIKTSYAGVKEKYLSEYCFSGTVIL	420
QY	421	SLLLOGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIIPAEQPLSTPLSHSTYVFL	480
DB	421	SLLLOGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIIPAEQPLSTPLSHSTYVFL	480
QY	481	MVLFSLVLTVAIIIGLIFHKP	502
DB	481	MVLFSLVLTVAIIIGLIFHKP	502

RESULT 9

US-09-835-147-27  
; Sequence 27, Application US/09835147  
; Patent No. US20020002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
; OTHER INFORMATION: construct of human CD39  
US-09-835-147-27

Query Match 87.4%; Score 2358; DB 9; Length 464;  
Best Local Similarity 97.8%; Pred. No. 4.5e-203;  
Matches 443; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY	24	SSIIATVIALAVGLTQNKALPENVKYIGVLDAGSSHTSLYIYKWPAREKNDGTGVHVEE	83
DB	12	SCIALSLATVNSATQNKALPENVKYIGVLDAGSSHTSLYIYKWPAREKNDGTGVHVEE	71
QY	84	CRVKGPGISKFQKNEIGIYLTDCMERAREVIPRSOHOETPVYLGATAGMRLRMESEE	143
DB	72	CRVKGPGISKFQKNEIGIYLTDCMERAREVIPRSOHOETPVYLGATAGMRLRMESEE	131
QY	144	LADRVLDVVERSLSNYPDFQGARIIITGQEGAYGWIITINYLKGFQSKTRWFSIVPYET	203
DB	132	LADRVLDVVERSLSNYPDFQGARIIITGQEGAYGWIITINYLKGFQSKTRWFSIVPYET	191
QY	204	NNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYKDYNNYTHSFLCYGKQDQALW	263
DB	192	NNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYKDYNNYTHSFLCYGKQDQALW	251
QY	264	OKLAKDIOVASNEILRDPCHFPGYKVVNSDLYKTPCTKRFEMTLPFOQFEIQIGNYQ	323
DB	252	OKLAKDIOVASNEILRDPCHFPGYKVVNSDLYKTPCTKRFEMTLPFOQFEIQIGNYQ	311
QY	324	QCHQSILELFNTSYCPYSQCAFNGIFLPLQDGFCAFSAFYFMKFLNLTSEKVSQEKVT	383
DB	312	QCHQSILELFNTSYCPYSQCAFNGIFLPLQDGFCAFSAFYFMKFLNLTSEKVSQEKVT	371
QY	384	EMMKKCAQWPBEIKTSYAGVKEKYLSEYCFSGTVILSLLLOGYHFTADSWEHIFIGIKI	443
DB	372	EMMKKCAQWPBEIKTSYAGVKEKYLSEYCFSGTVILSLLLOGYHFTADSWEHIFIGIKI	431
QY	444	QGSAGWTGLGYMLNTNMIIPAEQPLSTPLSHST	476
DB	432	QGSAGWTGLGYMLNTNMIIPAEQPLSTPLSHST	464

RESULT 10  
US-09-374-586-2  
; Sequence 2, Application US/09374586  
; Patent No. US20020138858A1  
; GENERAL INFORMATION:

```

; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match      87.0%; Score 2348; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 3.3e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGPISKFVOK 97
Db 1 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGPISKFVOK 60

QY 98 VNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 157
Db 61 VNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 120

QY 158 NYPDFQOGARIITGOEGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 217
Db 121 NYPDFQOGARIITGOEGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 180

QY 218 STQVTFVQNOTIESPDNALQRLYKGDYNNVTHSFLCYGKQDALWOKLAKDIOVASNEI 277
Db 181 STQVTFVQNOTIESPDNALQRLYKGDYNNVTHSFLCYGKQDALWOKLAKDIOVASNEI 240

QY 278 LRDPCHFPGYKVKVNVSDLYKTPCTKRPFMTLPFQOFEIQIGNYQOCHQSILELFNTSY 337
Db 241 LRDPCHFPGYKVKVNVSDLYKTPCTKRPFMTLPFQOFEIQIGNYQOCHQSILELFNTSY 300

QY 338 CPYSQAFNGIFLPPLOQDGFAGSAFYFVNMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397
Db 301 CPYSQAFNGIFLPPLOQDGFAGSAFYFVNMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 360

QY 398 KTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWHEHIFGKIQGS DAGTGLGYMLN 457
Db 361 KTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWHEHIFGKIQGS DAGTGLGYMLN 420

QY 458 LTNMIPAEQPLSTPLSHST 476
Db 421 LTNMIPAEQPLSTPLSHST 439

RESULT 11
US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match      87.0%; Score 2348; DB 9; Length 454;
Best Local Similarity 100.0%; Pred. No. 3.4e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGPISKFVOK 97
Db 16 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGPISKFVOK 75

QY 98 VNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 157
Db 76 VNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 135

QY 158 NYPDFQOGARIITGOEGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 217
Db 136 NYPDFQOGARIITGOEGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 195

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QY 278 LRDPCHFPGYKVKVNVSDLYKTPCTKRPFMTLPFQOFEIQIGNYQOCHQSILELFNTSY 337
Db 256 LRDPCHFPGYKVKVNVSDLYKTPCTKRPFMTLPFQOFEIQIGNYQOCHQSILELFNTSY 315

QY 338 CPYSQAFNGIFLPPLOQDGFAGSAFYFVNMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397
Db 316 CPYSQAFNGIFLPPLOQDGFAGSAFYFVNMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 375

QY 398 KTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWHEHIFGKIQGS DAGTGLGYMLN 457
Db 376 KTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWHEHIFGKIQGS DAGTGLGYMLN 435

QY 458 LTNMIPAEQPLSTPLSHST 476
Db 436 LTNMIPAEQPLSTPLSHST 454

RESULT 12
US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT

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; ORGANISM: Artificial Sequence		US-09-835-147-30	
; FEATURE:		Query Match 87.0%; Score 2348; DB 9; Length 463;	
; OTHER INFORMATION: Description of Artificial Sequence: Fusion		Best Local Similarity 100.0%; Pred. No. 3.5e-202;	
; OTHER INFORMATION: construct of human CD39		Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	25	TQNKALPENVKYGVILVDAGSSHTSLYIYKPAEKENDTGVVHVQVECRVKGGISKFVQK	84
QY	98	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVVERSLS	157
DB	85	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVVERSLS	144
QY	158	NYPDFQOGARIITQOEGAGYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGGA	217
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QY	218	STQVTFVPQNOTIESPDNALQRLYKGVNVDYTHSFLCYGKDQALWQKLAKDIOVASNEI	277
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QY	278	LRDPCFHPGYKKVNVSDLYKTPCTKRFEMTLPFQOFEIQGICNYQOCHQSILELFNFSY	337
DB	265	LRDPCFHPGYKKVNVSDLYKTPCTKRFEMTLPFQOFEIQGICNYQOCHQSILELFNFSY	324
QY	338	CPYSQCAFNGIFLPPLOQDGFAGSAFYFVKFNLNLTSEKVSQEKVTEMMKKFCAQPWBEI	397
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; Patent No. US20020002277A1			
; GENERAL INFORMATION:			
; APPLICANT: Maliszewski, Charles R.			
; APPLICANT: Gayle III, Richard B.			
; APPLICANT: Price, Virginia L.			
; APPLICANT: Gimpel, Steven D.			
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
; FILE REFERENCE: 2879-US			
; CURRENT APPLICATION NUMBER: US/09/835,147			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: US 60/104,585			
; PRIOR FILING DATE: 1998-10-16			
; PRIOR APPLICATION NUMBER: US 60/107,466			
; PRIOR FILING DATE: 1998-11-06			
; PRIOR APPLICATION NUMBER: US 60/149,010			
; PRIOR FILING DATE: 1999-08-13			
; PRIOR APPLICATION NUMBER: PCT/US99/22955			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 29			
; LENGTH: 473			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Fusion			
; OTHER INFORMATION: construct of human CD39			
US-09-835-147-28			
Query Match 87.0%; Score 2348; DB 9; Length 474;			
Best Local Similarity 100.0%; Pred. No. 3.7e-202;			
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
US-09-835-147-28			
QY	38	TQNKALPENVKYGVILVDAGSSHTSLYIYKPAEKENDTGVVHVQVECRVKGGISKFVQK	97
DB	35	TQNKALPENVKYGVILVDAGSSHTSLYIYKPAEKENDTGVVHVQVECRVKGGISKFVQK	94
QY	98	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVVERSLS	157
DB	95	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVVERSLS	154
QY	158	NYPDFQOGARIITQOEGAGYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGGA	217
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QY	218	STQVTFVPQNOTIESPDNALQRLYKGVNVDYTHSFLCYGKDQALWQKLAKDIOVASNEI	277
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QY	278	LRDPCFHPGYKKVNVSDLYKTPCTKRFEMTLPFQOFEIQGICNYQOCHQSILELFNFSY	337
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QY	338	CPYSQCAFNGIFLPPLOQDGFAGSAFYFVKFNLNLTSEKVSQEKVTEMMKKFCAQPWBEI	397
DB	335	CPYSQCAFNGIFLPPLOQDGFAGSAFYFVKFNLNLTSEKVSQEKVTEMMKKFCAQPWBEI	394
QY	398	KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFIGIKQSDAGWTIGYMLN	457
DB	395	KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFIGIKQSDAGWTIGYMLN	454
QY	458	LTNMIPAEQPLSTPLSHST	476
DB	455	LTNMIPAEQPLSTPLSHST	473
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; Sequence 28, Application US/09835147			
; Patent No. US20020002277A1			
; GENERAL INFORMATION:			
; APPLICANT: Maliszewski, Charles R.			
; APPLICANT: Gayle III, Richard B.			
; APPLICANT: Price, Virginia L.			
; APPLICANT: Gimpel, Steven D.			
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
; FILE REFERENCE: 2879-US			
; CURRENT APPLICATION NUMBER: US/09/835,147			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: US 60/104,585			
; PRIOR FILING DATE: 1998-11-06			
; PRIOR APPLICATION NUMBER: US 60/149,010			
; PRIOR FILING DATE: 1999-08-13			
; PRIOR APPLICATION NUMBER: PCT/US99/22955			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 28			
; LENGTH: 474			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Fusion			
; OTHER INFORMATION: construct of human CD39			
US-09-835-147-28			
Query Match 87.0%; Score 2348; DB 9; Length 474;			
Best Local Similarity 100.0%; Pred. No. 3.7e-202;			
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
US-09-835-147-28			





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Maximum Match 100%  
Listing first 45 summaries

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- 5: gb\_ov.\*
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- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_ats.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1365	100.0	1437	6	BD228700
3	1328	97.3	1464	6	BD228710
4	1319.2	96.6	1599	6	BD228698
5	1319.2	96.6	1704	9	HSU87967
6	1319.2	96.6	1818	6	AR168353
7	1319.2	96.6	1818	6	AR380930
8	1319.2	96.6	1818	6	AX828644
9	1319.2	96.6	1818	9	S73813
10	1319.2	96.6	2081	6	AX828400
11	1319.2	96.6	2081	9	HSN133133
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13	1319.2	96.6	3236	6	CQ870276
14	1319.2	96.6	3502	6	CQ870270
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25	703.2	51.5	1488	6	CQ870268	CQ870268 Sequence	
26	703.2	51.5	1815	9	HSN133134	AJ133134 Homo sapi	
C	27	640.2	46.9	704	6	AX828501	AX828501 Sequence
C	28	640.2	46.9	704	6	AX828547	AX828547 Sequence
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30	524.4	38.4	3211	5	BC076662	BC076662 Xenopus t	
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34	291	21.3	2783	6	CQ715235	CQ715235 Sequence	
35	291	21.3	2797	6	AR194793	AR194793 Sequence	
36	291	21.3	2797	6	AR562109	AR562109 Sequence	
37	291	21.3	2797	6	AR567207	AR567207 Sequence	
38	291	21.3	2797	6	AR567913	AR567913 Sequence	
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ALIGNMENTS

RESULT 1  
BD228699 1365 bp DNA linear PAT 17-JUL-2003  
LOCUS Inhibitors of platelet activation and recruitment.  
DEFINITION  
ACCESSION BD228699.1 GI:33038469  
VERSION JP 2002527096-A/2.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 1365)  
AUTHORS Maliszewski, C.R., Ili, R.B.G., Price, V.L. and Gimpe, S.D.  
TITLE Inhibitors of platelet activation and recruitment  
JOURNAL Patent: JP 2002527096-A 2 27-AUG-2002;  
IMMUNEX CORP  
COMMENT OS Artificial Sequence  
PN JP 2002527096-A/2  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185  
PR 16-OCT-1998 US 60/104585,06-NOV-1998 US 60/107466 PR  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI  
STEVEN D GIMPEL  
PC C12N15/09,A61K38/00,A61P9/00,C07K14/705,C12N1/15,C12N1/19, PC  
C12N5/10.  
PC C12P21/02/C12N9/14,C12N15/00,A61K37/02,C12N5/00 CC  
Description of Artificial Sequence: Fusion construct of human CC  
CD39

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FH Key Location/Qualifiers  
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Query Match 100.0%; Score 1365; DB 6; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS	BD228700	Inhibitors of platelet activation and recruitment.			
DEFINITION	BD228700	Inhibitors of platelet activation and recruitment.			
ACCESSION	BD228700.1	GI:33038470			
VERSION	JP 2002527096-A/3.				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 1437)				
AUTHORS	Maliszewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D.				
TITLE	Inhibitors of platelet activation and recruitment				
JOURNAL	Patent: JP 2002527096-A 3 27-AUG-2002;				
COMMENT	IMMUNEX CORP				
	OS	Artificial Sequence			
	PN	JP 2002527096-A/3			
	PD	27-AUG-2002			
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	PR	16-OCT-1998 US 60/104585, 06-NOV-1998 US 60/107466 PR			
	13-AUG-1999	US 60/149010			
	PI	CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI			
	STEVEN D GIMPEL				
	PC	C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC			
	C12N5/10,				
	PC	C12P21/02//C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC			
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Qy	121	TACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAGCGCTGGTGCATCAAGTAGAA	180		
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Db	313	ATTACTCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGATTTCAAAGTCCAGCACCAA	372
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Db	373	GAGACACCGTTTACTGTGGAGCCACGGCAGGCATGCGGTGCTCAGGATGAAAGTGAA	432
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Qy	421	TTTCAGGGTGCCAGGATCATTACTGCGCCAAAGGAAGGTGCCCTATGGCTGGATTACTATC	480
Db	493	TTTCAGGGTGCCAGGATCATTACTGCGCCAAAGGAAGGTGCCCTATGGCTGGATTACTATC	552
Qy	481	AACATATCTGTGGGCAAAATTCAGTCAGAAAAACAAGGTGGTTTCAGCATAGTCCCATGAA	540
Db	553	AACATATCTGTGGGCAAAATTCAGTCAGAAAAACAAGGTGGTTTCAGCATAGTCCCATGAA	612
Qy	541	ACCAATATCAGGAACCTTTGGAGCTTTGGACCTTTGGAGCCTTTGGAGCCTTTACACAAGTCACT	600
Db	613	ACCAATATCAGGAACCTTTGGAGCTTTGGAGCCTTTGGAGCCTTTGGAGCCTTTACACAAGTCACT	672
Qy	601	TTTGTACCCCAAAACAGACTATCCAGTCCCCAGATAATGCTCTGCAATTTTCGCCTCTAT	660
Db	673	TTTGTACCCCAAAACAGACTATCCAGTCCCCAGATAATGCTCTGCAATTTTCGCCTCTAT	732
Qy	661	GGCAAGGACTACAAATGTTCTACACATAGCTTTCTTGCTATGGGAAGGATCAGGACATC	720
Db	733	GGCAAGGACTACAAATGTTCTACACATAGCTTTCTTGCTATGGGAAGGATCAGGACATC	792
Qy	721	TGGCAGAAACTGGCCCAAGGACATTCAGTTGCAAGTAAATGAAATTTCTCAGGGAACCATGC	780
Db	793	TGGCAGAAACTGGCCCAAGGACATTCAGTTGCAAGTAAATGAAATTTCTCAGGGAACCATGC	852
Qy	781	TTTTCATCTCGGATATAAGAAAGTGTAGTGAACGTAAAGTGAACCTTTTACAAGACCCCTGCAC	840
Db	853	TTTTCATCTCGGATATAAGAAAGTGTAGTGAACGTAAAGTGAACCTTTTACAAGACCCCTGCAC	912
Qy	841	AAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAGGGTATTTGGAAACTAT	900
Db	913	AAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAGGGTATTTGGAAACTAT	972
Qy	901	CAACATGCCATCAAGAGATCTGTGAGCTCTTCAACACCGATTACTGCCCTTTACTCCGAC	960
Db	973	CAACAAATGCCATCAAGAGATCTGTGAGCTCTTCAACACCGATTACTGCCCTTTACTCCGAC	1032
Qy	961	TGTGCTTTCAATGGATTTTCTTGCCACACTCCAGGGGGATTTTGGGGCATTTTTCAGCT	1020
Db	1033	TGTGCTTTCAATGGATTTTCTTGCCACACTCCAGGGGGATTTTGGGGCATTTTTCAGCT	1092
Qy	1021	TTTTACTTTGTGATGAAGTTTAAAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGTG	1080
Db	1093	TTTTACTTTGTGATGAAGTTTAAAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGTG	1152
Qy	1081	ACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAAAACATCTTACGCT	1140
Db	1153	ACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAAAACATCTTACGCT	1212
Qy	1141	GGAGTAAAGGAGAGTACCTCAGTGAATACTGCTTTTCTGCTACTACATCTCTCCCTC	1200
Db	1213	GGAGTAAAGGAGAGTACCTCAGTGAATACTGCTTTTCTGCTACTACATCTCTCCCTC	1272
Qy	1201	CTTCTGCAAGGCTATCATTTTCAACAGCTGATTTCTGGGAGCACATCCCATTTTCAATTTGGCAAG	1260
Db	1273	CTTCTGCAAGGCTATCATTTTCAACAGCTGATTTCTGGGAGCACATCCCATTTTCAATTTGGCAAG	1332
Qy	1261	ATCAGGGCAGCGACGCGGCTGGAATTTGGGCTACATGCTGGAACCTGACCAACATGATC	1320

Db	1333	ATCCAGGCGCAGCGACGCGGCTGGAGCTTTGGGCTATACGTGTGAACCTTGACCAACATGATC	1399
Qy	1321	CCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTTCCACCTAA	1365
Db	1393	CCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTTCCACCTAA	1437
RESULT 3			
BD228710			
LOCUS	BD228710	1464 bp	DNA linear
DEFINITION	Inhibitors of platelet activation and recruitment.		
ACCESSION	BD228710		
VERSION	BD228710.1	GI:33038480	
KEYWORDS	JP 2002527096-A/13.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	other sequences; artificial sequences.		
AUTHORS	1 (bases 1 to 1464)		
TITLE	Maliszewski,C.R., Ili,R.B.G., Price,V.L. and Gimpe,S.D.		
JOURNAL	Inhibitors of platelet activation and recruitment		
COMMENT	Patent: JP 2002527096-A 13 27-AUG-2002;		
	IMMUNEX CORP		
	OS Artificial Sequence		
	PN JP 2002527096-A/13		
	PD 27-AUG-2002		
	PR 13-OCT-1999 JP 2000577185		
	PR 16-OCT-1998 US 60/104585,06-NOV-1998 US 60/107466 PR		
	13-AUG-1999 US 60/149010		
	PI CHARLES R MALISZEWSKI,RICHARD B GAYLE III,VIRGINIA L PRICE,PI		
	STEVEN D GIMPEL		
	PC C12N15/09,A61K38/00,A61P9/00,C07K14/705,C12N1/15,C12N1/19,PC		
	C12N5/10,		
	PC C12P21/02//C12N9/14,C12N15/00,A61K37/02,C12N5/00 CC		
	Description of Artificial Sequence: Fusion construct of human CC		
	CD39		
FEATURES			
source			
ORIGIN			
Query Match	97.3%;	Score 1328;	DB 6; Length 1464;
Best Local Similarity	98.5%;	Pred. No. 0;	
Matches 1334;	Conservative	0; Mismatches	21; Indels 0; Gaps 0;
Qy	11	CAAGTTTCTCAAAAGAAAACACAGCTAACTAGTTTCAACCCAGAACAAAGCATTTGCCAGAAA	70
Db	110	CTAGTTTCAGGAGACTACAAAGATGACGATGACAAAAACCCAGAACAAAGCATTTGCCAGAAA	169
Qy	71	ACGTTAAGTATGGATTTGCTGGATGCGGGTCTTCTTCCACACAAGTTTATACATCTATA	130
Db	170	ACGTTAAGTATGGATTTGCTGGATGCGGGTCTTCTTCCACACAAGTTTATACATCTATA	229
Qy	131	AGTGGCCAGCAGAAAAAGGAGAATGACACAGGGCTGTGCATCAAGTAGAAGAAATGACAGG	190
Db	230	AGTGGCCAGCAGAAAAAGGAGAATGACACAGGGCTGTGCATCAAGTAGAAGAAATGACAGG	289
Qy	191	TTAAAGGCTCTGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAAATAGGCATTTTACCTGA	250
Db	290	TTAAAGGCTCTGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAAATAGGCATTTTACCTGA	349
Qy	251	CTGATTGCATGGAAAGAGCTTAGGAAAGTGAATTTCCAAAGTCCCGACCAAGAGACACCCCG	310
Db	350	CTGATTGCATGGAAAGAGCTTAGGAAAGTGAATTTCCAAAGTCCCGACCAAGAGACACCCCG	409
Qy	311	TTTACCTGGGAGCCAGCGCAGGCATCGCGTCTCAGGATGGAAGTGAAGATTGGCAG	370
Db	410	TTTACCTGGGAGCCAGCGCAGGCATCGCGTCTCAGGATGGAAGTGAAGATTGGCAG	469
Qy	371	ACAGGGTTCTCGATGTGGTGGAGAGAGAGCCCTCAGCAACCTTACCCCTTTTGACTTTCCAGGGTG	430

Db	470		ACAGGTTCTGGATGTGGTGAGAGAGGCTCAGCAACTACCCCTTGACTTCCAGGGTG	529
Qy	431		CCAGGATCATTAATCGGCCAAGAGAGGTCCTATCGCTGGATTAATCAATCAATCTCTGC	490
Db	530		CCAGGATCATTAATCGGCCAAGAGAGGTCCTATCGCTGGATTAATCAATCAATCTCTGC	589
Qy	491		TGGGCAATTCAGTCAAGAAACAGGTGGTTCAGCATAGTCCCATATGAACCAATAATC	550
Db	590		TGGGCAATTCAGTCAAGAAACAGGTGGTTCAGCATAGTCCCATATGAACCAATAATC	649
Qy	551		AGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACTTTGTACCCC	610
Db	650		AGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACTTTGTACCCC	709
Qy	611		AAACAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTCCCTCTATGCAAGACT	670
Db	710		AAACAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTCCCTCTATGCAAGACT	769
Qy	671		ACAATGCTACACATAGTCTTCTGCTATGCGAAGGATCAGCACTCTGCGAAGAC	730
Db	770		ACAATGCTACACATAGTCTTCTGCTATGCGAAGGATCAGCACTCTGCGAAGAC	829
Qy	731		TGCCCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGCTTTTCATCTG	790
Db	830		TGCCCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGCTTTTCATCTG	889
Qy	791		GATATAAGAGGTAAGTAAGTGAAGTCACTTTTACAAGACCCCTGCAACAAGAGATTG	850
Db	890		GATATAAGAGGTAAGTAAGTGAAGTCACTTTTACAAGACCCCTGCAACAAGAGATTG	949
Qy	851		AGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATGGAACTATCAACATGCC	910
Db	950		AGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATGGAACTATCAACATGCC	1009
Qy	911		ATCAAGACATCTCGAGCTCTTCAACACCAAGTACTGCCCCCTTACTCCAGTGTGCCCTTCA	970
Db	1010		ATCAAGACATCTCGAGCTCTTCAACACCAAGTACTGCCCCCTTACTCCAGTGTGCCCTTCA	1069
Qy	971		ATGGGATTTTTCGCCACCACTCCAGGGGATTTTGGGGCATTTTCAGCTTTTACTTTTG	1030
Db	1070		ATGGGATTTTTCGCCACCACTCCAGGGGATTTTGGGGCATTTTCAGCTTTTACTTTTG	1129
Qy	1031		TGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGA	1090
Db	1130		TGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGA	1189
Qy	1091		TGAAAGATTTCTGTGCTCAGCCTTGGAGGAGATAAAACATCTTACGCTGGAGTAAAG	1150
Db	1190		TGAAAGATTTCTGTGCTCAGCCTTGGAGGAGATAAAACATCTTACGCTGGAGTAAAG	1249
Qy	1151		AGAAGTACCTGAGTGAATACGTCTTCTGGTACCTACATCTCTCCCTCTCTGCAAG	1210
Db	1250		AGAAGTACCTGAGTGAATACGTCTTCTGGTACCTACATCTCTCCCTCTCTGCAAG	1309
Qy	1211		GCTATCATTTACAGCTGATTTCTGGAGCAGATCCATTTTCATTTGGCAGATCCAGGCA	1270
Db	1310		GCTATCATTTACAGCTGATTTCTGGAGCAGATCCATTTTCATTTGGCAGATCCAGGCA	1369
Qy	1271		GCACGCGGCTGACTTTTGGGCTACATGCTGAACTGACCAACATGATCCCACTGAGC	1330
Db	1370		GCACGCGGCTGACTTTTGGGCTACATGCTGAACTGACCAACATGATCCCACTGAGC	1429
Qy	1331		AACCATTTGCCACCTCTCTCCACTCCACTTAA	1365
Db	1430		AACCATTTGCCACCTCTCTCCACTCCACTTAA	1464

RESULT 4  
BD228698  
LOCUS  
DEFINITION Inhibitors of platelet activation and recruitment.  
ACCESSION BD228698  
PAT 17-JUL-2003

VERSION	BD228698.1	GI:33038468
KEYWORDS	JP 2002527096-A/1	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1 (bases 1 to 1599)	
AUTHORS	Mallizewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D.	
TITLE	Inhibitors of platelet activation and recruitment	
JOURNAL	Patent: JP 2002527096-A 1 27-AUG-2002;	
IMMUNEX CORP		
COMMENT	OS Homo sapiens (human) PN JP 2002527096-A/1 PD 27-AUG-2002 PF 13-OCT-1999 JP 2000577185 PR 16-OCT-1998 US 60/104585, 06-NOV-1998 US 60/107466 PR 13-AUG-1999 US 60/149010 PI CHARLES R MALIJSZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI STEVEN D GIMPEL PC C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC C12N5/10, PC C12P21/02//C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC Inhibitors of platelet activation and recruitment PH Key Location/Qualifiers FT CDS (67)..(1596).	
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source	1..1599	
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	/mol_type="genomic DNA"	
	/db_xref="taxon:9606"	
ORIGIN		
Query Match	96.6%;	Score 1319.2; DB 6; Length 1599;
Best Local Similarity	99.8%;	Pred. No. 0;
Matches 1321; Conservative	0; Mismatches	3; Indels 0; Gaps 0;
Qy	41	GTTCACCAAGCAAAAGCAATTCGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATCGCG 100
Db	173	GGTTGACCCAGAAACAAAGCAATTCGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATCGCG 232
Qy	101	GTTCCTTCTCACACAAGTTTATATCATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 160
Db	233	GTTCCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 292
Qy	161	GGTGGTGTGATCACTAGTAGAAGTCCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220
Db	293	GGTGGTGTGATCAAGTAGAAGTCCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 352
Qy	221	AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTCGATGGAAAGAGCTAGGGAAGTGA 280
Db	353	AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTCGATGGAAAGAGCTAGGGAAGTGA 412
Qy	281	TTCCAAGTCCAGACCAAGACACCCGTTTACCTGGGAGCCACGGCAGGCGATCGGTT 340
Db	413	TTCCAAGTCCAGACCAAGACACCCGTTTACCTGGGAGCCACGGCAGGCGATCGGTT 472
Qy	341	TGCTCAGGATGGAAAGTGAAGTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 400
Db	473	TGCTCAGGATGGAAAGTGAAGTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 532
Qy	401	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCCCAAGAGAGAGGTG 460
Db	533	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCCCAAGAGAGAGGTG 592
Qy	461	CTATGGCTGGATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAAAGGTGTT 520
Db	593	CTATGGCTGGATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAAAGGTGTT 652
Qy	521	TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 580
Db	653	TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 712
Qy	581	GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGAGACTATCGAGTCCCCAGATAATG 640

Db	713	GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACCAAGACTATCGAGTCCCAGATAATG	772
Qy	641	CTCTGCAATTTTGCCTCTATGCGCAAGGACTACAAATGTCTACACACATAGCTTCTTTGTGCT	700
Db	773	CTCTGCAATTTTGCCTCTATGCGCAAGGACTACAAATGTCTACACACATAGCTTCTTTGTGCT	832
Qy	701	ATGGGAAGGATCAGGACACTCTGGCAGAAAACCTGGCCAAAGGACATTCAGGTTGCAAGTAATG	760
Db	833	ATGGGAAGGATCAGGACACTCTGGCAGAAAACCTGGCCAAAGGACATTCAGGTTGCAAGTAATG	892
Qy	761	AAATTTCTCAGGGACCCATGCTTTTCATCCTCGATATAGAAGGTAGTGAACGTAAAGTGACC	820
Db	893	AAATTTCTCAGGGACCCATGCTTTTCATCCTCGATATAGAAGGTAGTGAACGTAAAGTGACC	952
Qy	821	TTTACAAGACCCCTGCGACCAAGAGATTTTGAGATGACTCTTCCATTCACAGCAGTTTGGAAA	880
Db	953	TTTACAAGACCCCTGCGACCAAGAGATTTTGAGATGACTCTTCCATTCACAGCAGTTTGGAAA	1012
Qy	881	TCCAGGATATGGAAAATATCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCA	940
Db	1013	TCCAGGATATGGAAAATATCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCA	1072
Qy	941	GTTACTGCCCTTACTCCAGTGTCCTTCAATGGGATTTTCTGGCCACCACTCCAGGGGG	1000
Db	1073	GTTACTGCCCTTACTCCAGTGTCCTTCAATGGGATTTTCTGGCCACCACTCCAGGGGG	1132
Qy	1001	ATTTTGGGGCATTTTTCAGCTTTTTCATCTTCTGATGAAGTTTAACTTCACATCAGAGA	1060
Db	1133	ATTTTGGGGCATTTTTCAGCTTTTTCATCTTCTGATGAAGTTTAACTTCACATCAGAGA	1192
Qy	1061	AACTCTCTCAGGAAAAGGTGACTGAGATGATGAAGAAAGTTTCTGTGCTCAGCCTTGGGAGG	1120
Db	1193	AACTCTCTCAGGAAAAGGTGACTGAGATGATGAAGAAAGTTTCTGTGCTCAGCCTTGGGAGG	1252
Qy	1121	AGATAAAACATCTTACGCTGGAGTAAGAGAGAAAGTACCTGAGTGAATATCTGCTTTCTG	1180
Db	1253	AGATAAAACATCTTACGCTGGAGTAAGAGAGAAAGTACCTGAGTGAATATCTGCTTTCTG	1312
Qy	1181	GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGCGGAGC	1240
Db	1313	GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGCGGAGC	1372
Qy	1241	ACATCCATTTTCATTTGGCAAGATCCAGGCGACGACCGCGCTGGACTTTGGGCTACATGC	1300
Db	1373	ACATCCATTTTCATTTGGCAAGATCCAGGCGACGACCGCGCTGGACTTTGGGCTACATGC	1432
Qy	1301	TGAACCTGACCAACATGATGCCAGCTGAGCAACATTTGTCACACCTCTCTTCCACTCCA	1360
Db	1433	TGAACCTGACCAACATGATGCCAGCTGAGCAACATTTGTCACACCTCTCTTCCACTCCA	1492
Qy	1361	CCTA 1364	
Db	1493	CCTA 1496	
RESULT 5			
LOCUS	HSU87967	1704 bp	PRI 18-FEB-1997
DEFINITION	Human ATP diphosphohydrolase mRNA, complete cds.		
ACCESSION	U87967		
VERSION	U87967.1		
KEYWORDS	GI:1842119		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (base 1 to 1704)		
JOURNAL	Kaczmarek, E., Koziak, K., Seigny, J., Siegel, J.B., Anrather, J.,		
	Beaudoin, A.R., Bach, F.H. and Robson, S.C.		
	Identification and characterization of CD39/vascular ATP		
	diphosphohydrolase		
	J. Biol. Chem. 271 (51), 33116-33122 (1996)		

QY 461 CCTATGGCTGATTACTATCACTATCTGCTGGSCAAATTCAGTCAGAAAAACAAGTGGT 520  
DB 557 CCTATGGCTGGATTACTATCACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 616  
QY 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
DB 617 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 676  
QY 581 GAGCCTCTACACAAGTCACCTTTGTATGCCCAAAACCGAGCTATCGAGTCCCGCAGATAATG 640  
DB 677 GAGCCTCTACACAAGTCACCTTTGTATGCCCAAAACCGAGCTATCGAGTCCCGCAGATAATG 736  
QY 641 CTCTGCAATTTCCGCTCTATGGCAAGGACTACATATGCTACACACATAGCTTCTGTGCT 700  
DB 737 CTCTGCAATTTCCGCTCTATGGCAAGGACTACATATGCTACACACATAGCTTCTGTGCT 796  
QY 701 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTTGCAAGTAATG 760  
DB 797 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTTGCAAGTAATG 856  
QY 761 AAATTTCTCAGGACCCATGCTTTCACTCTGGATATAGAAGGTAGTGAAGTGAAGTGAAC 820  
DB 857 AAATTTCTCAGGACCCATGCTTTCACTCTGGATATAGAAGGTAGTGAAGTGAAGTGAAC 916  
QY 821 TTTTACAAGACCCCTGACCAAGAGATTTGAGATGACTCTTCCAATCCAGCAGTTTGAAG 880  
DB 917 TTTTACAAGACCCCTGACCAAGAGATTTGAGATGACTCTTCCAATCCAGCAGTTTGAAG 976  
QY 881 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAAGCATCTCGAGACTTCCAACACCA 940  
DB 977 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAAGCATCTCGAGACTTCCAACACCA 1036  
QY 941 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTTGGCAACCATCCAGGGGG 1000  
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QY 1001 ATTTTGGGGCATTTTCAGCTTTTACTTTCTGTGATGAAGTTTAACTTGACATCAGAGA 1060  
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QY 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTCTGTGCTCAGCCTTTGGGAGG 1120  
DB 1157 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTCTGTGCTCAGCCTTTGGGAGG 1216  
QY 1121 AGATATAAAACATCTTACGCTGGAGTAAAGGAGAACTACCTGAGTGAATACCTGCTTTCTG 1180  
DB 1217 AGATATAAAACATCTTACGCTGGAGTAAAGGAGAACTACCTGAGTGAATACCTGCTTTCTG 1276  
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QY 1301 TGAACCTGACCAACATGATCCAGCTGAGAACCATTTGTCCACACCTCTCTCCACTCCA 1360  
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QY 1361 CCTA 1364  
DB 1457 CCTA 1460

RESULT 6  
LOCUS AR168353  
DEFINITION Sequence 2 from patent US 6287837.  
ACCESSION AR168353  
VERSION AR168353.1  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1818)  
AUTHORS Beaudoin,A.R. and Sevigny,J.  
TITLE Mammalian ATP-diphosphohydrolases and process of purification thereof  
JOURNAL Patent: US 6287837-A 2 11-SEP-2001;  
FEATURES Location/Qualifiers  
          source 1..1818  
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ORIGIN  
Query Match 96.6%; Score 1319.2; DB 6; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAAGCTTTAAGTATGGGATTTGCTGGATCGG 100  
DB 174 GGTTGACCCAGAACAAAGCATTTGCCAGAAAAAGCTTTAAGTATGGGATTTGCTGGATCGG 233  
QY 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAATGACACAG 160  
DB 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAATGACACAG 293  
QY 161 GCGTGGTGCATCAAGTAGAAGATGCAGGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTC 220  
DB 294 GCGTGGTGCATCAAGTAGAAGATGCAGGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTC 353  
QY 221 AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTTGCATGGAAAAAGAGCTAGGGAAGTGA 280  
DB 354 AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTTGCATGGAAAAAGAGCTAGGGAAGTGA 413  
QY 281 TTCCAAGTCCAGACCAAGAGACACCCGTTTACCTGGAGCCAGCGCAGGCAATCCGGT 340  
DB 414 TTCCAAGTCCAGACCAAGAGACACCCGTTTACCTGGAGCCAGCGCAGGCAATCCGGT 473  
QY 341 TGCTCAGGATGAAAGTGAAGATTTGGCAGACAGGGTTCTCGATGTGTGGAGAGAGGCC 400  
DB 474 TGCTCAGGATGAAAGTGAAGATTTGGCAGACAGGGTTCTCGATGTGTGGAGAGAGGCC 533  
QY 401 TCAGAACTTACCCCTTTTGACTTTCCAGGGTCCAGGATCAATTAATCGGCCAAGAGGAAGTGG 460  
DB 534 TCAGAACTTACCCCTTTTGACTTTCCAGGGTCCAGGATCAATTAATCGGCCAAGAGGAAGTGG 593  
QY 461 CTTATGGCTGGATTAATCAATATCTCTGGGCAAAATTCAGTCAAGAAAAAGTGGT 520  
DB 594 CTTATGGCTGGATTAATCAATATCTCTGGGCAAAATTCAGTCAAGAAAAAGTGGT 653  
QY 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
DB 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 713  
QY 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCCAGACTATCGAGTCCCGCAGATAATG 640  
DB 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCCAGACTATCGAGTCCCGCAGATAATG 773  
QY 641 CTCTGCAATTTCCGCTCTATGGCAAGGACTACATATGCTTACACACATAGCTTCTGTGCT 700  
DB 774 CTCTGCAATTTCCGCTCTATGGCAAGGACTACATATGCTTACACACATAGCTTCTGTGCT 833  
QY 701 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTTGCAAGTAATG 760  
DB 834 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTTGCAAGTAATG 893  
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QY	881	TCAGGGTATTGGAAACTATCAACAATGCCATCAAAAGCATCTCGGAGCTCTTCAACACCA	940
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QY	1001	ATTTTGGGGCATTTTTCAGCTTTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA	1060
Db	1134	ATTTTGGGGCATTTTTCAGCTTTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA	1193
QY	1061	AAGTCTCTCAGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG	1120
Db	1194	AAGTCTCTCTCAGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG	1253
QY	1121	AGATAAAAAACATCTTACGCTCGAGTAAAGGAGAGTACCTGAGTGAATACCTGCTTTTCTG	1180
Db	1254	AGATAAAAAACATCTTACGCTCGAGTAAAGGAGAGTACCTGAGTGAATACCTGCTTTTCTG	1313
QY	1181	GTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTCTGGGAGC	1240
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QY	1241	ACATCCATTTTCAATTTGGCAAGATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATGC	1300
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QY	1301	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA	1360
Db	1434	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA	1493
QY	1361	CCTA 1364	
Db	1494	CCTA 1497	
RESULT 7			
AR380930			
LOCUS	AR380930	1818 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 1475 from patent US 6607879.		
ACCESSION	AR380930		
VERSION	AR380930.1 GI:40088564		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1818)		
AUTHORS	Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.		
TITLE	Compositions for the detection of blood cell and immunological response gene expression		
JOURNAL	Patent: US 6607879-A 1475 19-AUG-2003;		
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QY	41	GTTCAACCCAGAACAAAGCATTTGCCAGAAACGTTTAAGTATGGGATTTGCTCGATCGG	100
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QY	101	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAAATGACACAG	160
Db	234	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAAATGACACAG	293
QY	161	CGGTGGTGCATCAAGTAGAAGATGCAAGGTTAAAGGTCCTCGGAATCTCAAAATTTGTTTC	220

Db	294	GGTGGTGCATCAAGTAGAAGATCGAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC	353
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Db	354	AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTTGATGCAAGAGAGCTAGGGAAGTGA	413
QY	281	TTCCAAGGTCCAGACCAAGAGACACCCGTTTACTCTGGAGGCCACGGCAGGATCGCGT	340
Db	414	TTCCAAGGTCCAGACCAAGAGACACCCGTTTACTCTGGAGGCCACGGCAGGATCGCGT	473
QY	341	TGCTCAGAGTGGAAAGTGAAGGTTGGCAGACAGGTTTCTGGATCTGTGGTGGAGAGAGCC	400
Db	474	TGCTCAGAGTGGAAAGTGAAGGTTGGCAGACAGGTTTCTGGATCTGTGGTGGAGAGAGCC	533
QY	401	TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTGCCCAGGAAGAGTG	460
Db	534	TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTGCCCAGGAAGAGTG	593
QY	461	CCTATGGCTGGATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGCAAAAAACAAGTGCT	520
Db	594	CCTATGGCTGGATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGCAAAAAACAAGTGCT	653
QY	521	TCAGATAGTCCCATATGAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTGGGG	580
Db	654	TCAGATAGTCCCATATGAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTGGGG	713
QY	581	GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCAGATCCCCAGATAATG	640
Db	714	GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCAGATCCCCAGATAATG	773
QY	641	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGCT	700
Db	774	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGCT	833
QY	701	ATGGAGGATCAGGCACTCTGGCAGAACTGGGCCAAGGACATTCAGCTTGCAGATTAATG	760
Db	834	ATGGAGGATCAGGCACTCTGGCAGAACTGGGCCAAGGACATTCAGCTTGCAGATTAATG	893
QY	761	AAATTTCTCAGGAGCCATGCTTTTCATCTGGATATAAGAAAGTGTAGTGAACGTAGACC	820
Db	894	AAATTTCTCAGGAGCCCATGCTTTTCATCTGGATATAAGAAAGTGTAGTGAACGTAGACC	953
QY	821	TTTACAAGACCCCTGACCAAGAGATTGAGATGACTCTTCCATTCAGCAGATTTTGA	880
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QY	881	TCCAGGTTATTGGAACTATCAACAATGCCATCAAAAGCATCTCGAGCTCTTCAACACCA	940
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QY	941	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCCACCATCTCCAGGGG	1000
Db	1074	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCCACCATCTCCAGGGG	1133
QY	1001	ATTTTGGGGCATTTTCAGCTTTTTTACTTTTGATGAAGTTTTTAAACTTTGACATCAGAGA	1060
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QY	1061	AACTCTCTCAGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCTTGGGAGG	1120
Db	1194	AACTCTCTCAGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCTTGGGAGG	1253
QY	1121	AGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACTCTCAGTGAATACCTGCTTTCTG	1180
Db	1254	AGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACTCTCAGTGAATACCTGCTTTCTG	1313
QY	1181	GTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTCAAGCTGATTTCTTGGGAGC	1240
Db	1314	GTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTCAAGCTGATTTCTTGGGAGC	1373
QY	1241	ACATCCATTTTCAATGGGCAAGATCCAGGCGAGCGAGCCGGCTTGGGCTACATGC	1300
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QY 1361 CCTA 1364  
Db 1494 CCTA 1497  
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LOCUS AX828644 1818 bp DNA linear PAT 12-DEC-2003  
DEFINITION Sequence 290 from Patent WO03074073.  
ACCESSION AX828644  
VERSION AX828644.1 GI:39838595  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Al-Mahmood, S., Colin, S. and Schneider, C.  
TITLE Genes involved in regulating angiogenesis, pharmaceutical  
preparations containing same and applications thereof  
JOURNAL Patent: WO 03074073-A 290 12-SEP-2003;  
Gene Signal (FR)  
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1. 1818  
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Best Local Similarity 99.8%; Pred. No. 0;  
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QY 1361 CCTA 1364  
Db 1494 CCTA 1497  
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S73813  
LOCUS S73813 1818 bp mRNA linear PRI 12-APR-1995  
DEFINITION CD39=lymphoid cell activation antigen [human, B lymphoblastoid cell  
line, MP-1, mRNA, 1818 nt].  
ACCESSION S73813  
VERSION S73813.1 GI:765255  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1818)  
AUTHORS Maliszewski, C.R., Delespesse, G.J., Schoenborn, M.A., Armitage, R.J.,  
Fanslow, W.C., Nakajima, T., Baker, E., Sutherland, G.R.,

TITLE Poindexter, K., Birks, C. et, al.  
The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization  
J. Immunol. 153 (8), 3574-3583 (1994)  
MEDLINE 95015846  
PUBMED 7930580  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gisegg 156681] from the original journal article.  
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gene source

CDS

ORIGIN

Query Match 96.6%; Score 1319.2; DB 9; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	41	GTTCAACCCAGAACAAAGCATTCAGAGAAACGTTAAAGTATCGGATTCGCTGGATCGG	100
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QY	101	GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGGAATGACACAG	160
DB	234	GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGGAATGACACAG	293
QY	161	GGTGGTGCATCAAGTAGAAGATGACAGGTTAAAGTCTTGGATCTCAAAATTTGTTTC	220
DB	294	GGTGGTGCATCAAGTAGAAGATGACAGGTTAAAGTCTTGGATCTCAAAATTTGTTTC	353
QY	221	AGAAAGTAAATCAATAGCATTTACCTGACTGATTCGATGCAAGAGAGCTAGGAGTGA	280
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QY	341	TGCTCAGATGAAAGTAGAGTTGGCAGACAGAGGTTCTGATGTGTGGAGAGAGCC	400
DB	474	TGCTCAGATGAAAGTAGAGTTGGCAGACAGAGGTTCTGATGTGTGGAGAGAGCC	533
QY	401	TCAGCAACTACCCCTTGACTTCCAGGTTGCCAGGATCATTTACTGGCCAGAGGAGGTG	460
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QY	461	CCTATGGCTGGATTACTTCAACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGGTGGT	520
DB	594	CCTATGGCTGGATTACTTCAACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGGTGGT	653
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DB	654	TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG	713
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DB	714	GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCAGAGTCCCCAGATAATG	773
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DB	774	CTCTCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTTCTTGCTGT	833
QY	701	ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACTTCAAGTTGCAAGTAATG	760
DB	834	ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACTTCAAGTTGCAAGTAATG	893
QY	761	AAATTTCTCAGGAGCCATGCTTTTCATCTGGATATAAGAAAGTGTAGTAACGTAAGTGACC	820
DB	894	AAATTTCTCAGGAGCCATGCTTTTCATCTGGATATAAGAAAGTGTAGTAACGTAAGTGACC	953
QY	821	TTTCAAGACCCCTTGCAACAGAGATTGAGATGACTTCTCCATTTCCAGCAGTTTGA	880
DB	954	TTTCAAGACCCCTTGCAACAGAGATTGAGATGACTTCTCCATTTCCAGCAGTTTGA	1013
QY	881	TCCAGGATTTGGAAACTATCAACATGCCATCAAGGACTCCTGAGCTTTCACACCA	940
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QY	941	GTTACTGCCCTTACTCCAGTGCTCTCAATGGGATTTCTTTCGCCACACCTCCAGGGGG	1000
DB	1074	GTTACTGCCCTTACTCCAGTGCTCTCAATGGGATTTCTTTCGCCACACCTCCAGGGGG	1133
QY	1001	ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA	1060
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QY	1181	GTACCTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCCAGCTGATTTCTGGGAGC	1240
DB	1314	GTACCTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCCAGCTGATTTCTGGGAGC	1373
QY	1241	ACATCCATTTTCTGGCAAGATCCAGGCGAGGAGCCGCTGGAGTCTGGGCTACATGC	1300
DB	1374	ACATCCATTTTCTGGCAAGATCCAGGCGAGGAGCCGCTGGAGTCTGGGCTACATGC	1433
QY	1301	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA	1360
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DEFINITION	Sequence 46 from Patent WO03074073.		
ACCESSION	AX828400		
VERSION	AX828400.1	GI:39838400	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	Al-Mahmood, S., Colin, S. and Schneider, C.		

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Qy	1061	AGTCTCTCAGGAAAGGTGACCTGAGATGATGAAGTTCGTGCTCAGCTTGGGAGG	1120
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Qy	1181	GTACCTACATTTCTCTCCCTCTTCTCTGCAAGGCTATCATTTACAGCTGATTCCTGGGAGC	1240
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Qy	1241	ACATCCATTTCAATTGCGCAGATCCAGGGCAGCCGCCGCTGGACTTTTGGGCTACATGC	1300
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Db	1571	TGNACTTGACCAACATGATCCCAAGTGGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA	1630
Qy	1361	CCTA 1364	
Db	1631	CCTA 1634	
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LOCUS		2081 bp	mRNA
DEFINITION		Homo sapiens mRNA for ecto-ATP diphosphohydrolase, isolate C1800.	PRI 19-JAN-2000
ACCESSION		AJ133133	
VERSION		AJ133133.1	GI:4741544
KEYWORDS		ecto-ATP diphosphohydrolase I; ecto-ATPase I; PleA 1 gene.	
SOURCE		Homo sapiens	
ORGANISM		Homo sapiens	
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DEFINITION Sequence 697 from Patent WO2004074320.  
ACCESSION CQ870276  
VERSION CQ870276.1 GI:51999880  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Morris,D.W., Morris,D.W. and Malandro,M.S.  
TITLE Novel therapeutic targets in cancer  
JOURNAL Patent: WO 2004074320-A 697 02-SEP-2004;  
Sagres Discovery, Inc. (US)  
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LOCUS Q870270  
DEFINITION Sequence 691 from Patent WO2004074320.  
ACCESSION Q870270  
VERSION Q870270.1 GI:51999877  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE	1	Morris, D.W., Morris, D.W. and Malandro, M.S. Novel therapeutic targets in cancer Patent: WO 2004074320-A 691 02-SEP-2004; Sagres Discovery, Inc. (US)
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REFERENCE 1  
AUTHORS Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,  
Mikita,T. and Tai,J.  
TITLE Genes expressed in foam cell differentiation  
JOURNAL Patent: WO 01/77389-A 242 18-OCT-2001;  
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15	1319.2	96.6	1818	12 ADK60414	Adk60414 Angiogene
16	1319.2	96.6	1818	12 ADK60715	Adk60715 Angiogene
17	1319.2	96.6	1818	12 ADP73338	Adp73338 CD39 lym
18	1319.2	96.6	2080	11 ADN95840	Adn95840 Human BEC
19	1319.2	96.6	2081	6 ABK83558	Abk83558 Human cDN
20	1319.2	96.6	2081	12 ADK60471	Adk60471 Angiogene

21	1319.2	96.6	2081	12 ADK60772	Adk60772 Angiogene
22	1319.2	96.6	2081	12 ADP73094	Adp73094 Angiogene
23	1319.2	96.6	2986	13 ABD32956	Abd32956 Human can
24	1319.2	96.6	3236	13 ABD32958	Abd32958 Human can
25	1319.2	96.6	3502	13 ABD32955	Abd32955 Human can
26	1319.2	96.6	4411	6 AAS94987	Aas94987 Human DNA
27	1305.2	95.6	3506	13 ABD32957	Abd32957 Human can
28	1287.4	94.3	3244	13 ACN42028	Acn42028 Human dia
29	1119.4	82.0	3165	13 ACN42029	Acn42029 Human dia
30	1039	76.1	1479	10 ADI62639	Adi62639 Human apo
31	835	61.2	2296	13 ABD32952	Abd32952 Mouse can
32	703.2	51.5	1488	13 ABD32954	Abd32954 Human can
33	640.2	46.9	704	12 ADK60271	Adk60271 Antisense
34	640.2	46.9	704	12 ADK60572	Adk60572 Antisense
35	640.2	46.9	704	12 ADP73195	Adp73195 Angiogene
36	640.2	46.9	6164	12 ADK60317	Adk60317 Angiogene
37	640.2	46.9	6164	12 ADK60618	Adk60618 Angiogene
38	640.2	46.9	6164	12 ADP73241	Adp73241 Angiogene
39	414	30.3	475	9 ACH37444	Ach37444 Human end
40	379	27.8	484	9 ACH35840	Ach35840 Human end
41	291	21.3	2797	3 AAA96067	Aaa96067 Human ect
42	291	21.3	2797	6 AAD31694	Aad31694 Human CD3
43	291	21.3	2797	6 ABK10350	Abk10350 DNA encod
44	291	21.3	2797	12 ADQ99443	Adq99443 Human CD3
45	291	21.3	2797	13 ADR69172	Adr69172 Human CD3

ALIGNMENTS

RESULT 1  
AAD00206  
ID AAD00206 standard; DNA; 1365 BP.

AC AAD00206;

DT 17-AUG-2000 (first entry)

DE Human soluble CD39 and IL2 N-terminus comprising fusion DNA construct.  
KW Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

CDS 1..1365

FT /\*tag= a /product= "Fusion protein of human Interleukin 2 (IL2) N-terminus and human soluble CD39 protein"

FT misc\_feature 1..45

FT /\*tag= b /note= "N-terminus of mature human interleukin 2 (IL2) "

FT misc\_feature 46..1362

FT /\*tag= c /note= "Coding region of human soluble CD39 (solCD39) "

XX WO200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US022955.

XX 16-OCT-1998; 98US-0104585P.

XX 06-NOV-1998; 98US-0107466P.

XX 13-AUG-1999; 99US-0149010P.



KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antitanginal; cardiant;  
KW cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; ss.  
OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
FH 1. 1365  
FT CDS /\*tag= a  
FT /product= "Human soluble CD39 protein"  
FT  
XX  
XX WO200023094-A2.  
XX  
XX 27-APR-2000.  
XX  
XX 13-OCT-1999; 99WO-US023641.  
XX  
XX 16-OCT-1998; 98US-0104585P.  
PR 06-NOV-1998; 98US-0107466P.  
PR 13-AUG-1999; 99US-0149010P.  
XX  
XX (IMV ) IMMUNEX CORP.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
XX Maliszewski CR, Gayle RB, Marcus AJ;  
XX  
XX WPI; 2000-339518/29.  
DR P-PSDB; AAY70890.  
XX  
XX Inhibiting platelet activation and recruitment, useful for treating a  
PT mammal suffering from unstable angina, myocardial infarction, stroke,  
PT coronary artery disease or injury, comprises administering soluble CD39  
PT polypeptides.  
XX  
XX Claim 10; Page 93-95; 118pp; English.  
XX  
XX The present cDNA sequence is a fusion construct encoding sol(soluble)CD39  
CC having apyrase activity. Fusion of 12 amino acids from the N-terminus of  
CC mature human IL2 to the solCD39 coding region results in high levels of  
CC both expression and activity in the supernatants of transfected cells.  
CC This is used in the treatment of unstable angina, myocardial infarction,  
CC stroke, coronary artery disease or injury, atherosclerosis, peripheral  
CC vascular occlusion, preclampsia, embolism, platelet-associated ischaemic  
CC disorder including lung ischaemia, coronary ischaemia and cerebral  
CC ischaemia, a thrombotic disorder including coronary artery thrombosis,  
CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery  
CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous  
CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.  
CC Soluble CD39 is also useful for preventing thrombus formation or  
CC reformation, occlusion, reocclusion, stenosis or restenosis of blood  
CC vessels or stroke  
XX  
XX Sequence 1365 BP; 394 A; 317 C; 319 G; 335 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1365; DB 3; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TTGCCAGAAAACGTTAAGTATGGGATGTGCTGGATGCGGGTCTTCTCACAAAGTTTA 120  
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481 AACTATCTGCTGGGCAAAATTCAGTCAGAAACAAAGTGTGTTTCAGCATAGTCCCATATGA 540  
541 ACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGGCTCTACACAACTCACT 600  
541 ACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGGCTCTACACAACTCACT 600  
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841 AAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATTTGGAAACTAT 900  
901 CAACAATGCCATCAAGCATCTTCAACACAGTACTGCGCTTACTCCAGC 960  
901 CAACAATGCCATCAAGCATCTTCAACACAGTACTGCGCTTACTCCAGC 960  
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1081 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGGAGATAAAAACATCTTACGCT 1140  
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1141 GGAGTAAAGGAGAGTACCTGAGTGAATATGCTTTTCTTGTTACTACATCTCTCCCTC 1200  
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1201 CTTCTGCAAGGCTATCATTTTCAGAGCTGATTTCTGGGAGGACATCCATTTTCAITGGCAAG 1260  
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QY 1261 ATCCAGGCGACGACCGCGCTGGACTTTGGGTACATGCTGAACCTGACCAACATGATC 1320  
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DB |||||||  
RESULT 3  
AAD00207  
ID AAD00207 standard; DNA; 1437 BP.  
XX  
AC AAD00207;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Human soluble CD39 fusion DNA construct, pIL2LsolCD39.  
XX  
KW Soluble CD39; human; apyrase activity; platelet activation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;  
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;  
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;  
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;  
KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1437  
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FT /product= "Fusion protein of pIL2LsolCD39"  
FT sig\_peptide 1..72  
FT /\*tag= b  
FT /note= "Human interleukin 2 (hIL2) leader sequence"  
FT misc\_feature 73..108  
FT /\*tag= c  
FT /product= "Mature human interleukin 2 N-terminal end"  
FT misc\_feature 109..117  
FT /\*tag= d  
FT /note= "Linker sequence"  
FT misc\_feature 118..1434  
FT /\*tag= e  
FT /note= "Coding region of human soluble CD39 (solCD39)"  
XX  
PN WO200023459-A1.  
XX  
PD 27-APR-2000.  
XX  
PF 13-OCT-1999; 99WO-US022955.  
XX  
PR 16-OCT-1998; 98US-0104585P.  
PR 06-NOV-1998; 98US-0107466P.  
PR 13-AUG-1999; 99US-0149010P.  
XX  
PA (IMMUNEX ) IMMUNEX CORP.  
XX  
PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;  
XX  
DR WPI; 2000-339644/29.  
DR P-PSDB; AAY70914.  
XX  
PT New soluble CD39 polypeptides having apyrase activity, useful for  
PT inhibiting angiogenesis and treating unstable angina, myocardial  
PT infarction, stroke, coronary artery disease or injury.  
XX  
PS Claim 15a; Page 97-99; 122pp; English.  
XX  
CC The present DNA sequence is a fusion construct pIL2LsolCD39, comprising  
CC leader peptide of human interleukin 2 (hIL2), 12 amino acids from the

CC mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region,  
CC having apyrase activity. This produces high levels of solCD39 expression  
CC and activity in the transfected cells. Soluble CD39 is constructed by  
CC removing the N- and C-terminal transmembrane domains. It retains the  
CC capacity to metabolise ATP and ADP at relevant concentrations and the  
CC ability to block and reverse ADP-induced platelet activation and  
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides  
CC are useful for inhibiting angiogenesis. It is useful for the treatment of  
CC unstable angina, myocardial infarction, stroke, coronary artery disease  
CC or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia,  
CC embolism, platelet-associated ischaemic disorders including lung,  
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,  
CC peripheral and cerebral artery thrombosis, intracardiac and venous  
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
CC stenosis or restenosis of blood vessels or stroke  
XX  
SQ Sequence 1437 BP; 411 A; 336 C; 335 G; 355 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1365; DB 3; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 121 TACATCTATAGTGGCCAGAGAAAGGAGATGACACAGGCGTGGTGCATCAAGTAGAA 180  
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QY 181 GAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTCAAAAAGTAAATGAAATAGGC 240  
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QY 301 GAGACACCCGTTTACCTGGAGCCACGCGCAGCATGCGTTCCTCAGGATGAAAGTAGAA 360  
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QY 373 GAGACACCCGTTTACCTGGAGCCACGCGCAGCATGCGTTCCTCAGGATGAAAGTAGAA 432  
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QY 361 GAGTTGGCAGACAGGGGTTCTGGATGTGGTGGAGAGAGCCTCAGCAACTACCCCTTTGAC 420  
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QY 433 GAGTTGGCAGACAGGGGTTCTGGATGTGGTGGAGAGAGCCTCAGCAACTACCCCTTTGAC 492  
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QY 421 TTCCAGGGTGCAGGATCAATTACTGGCCAAAGGAGGTTGCCTATGGCTGGATTACTATC 480  
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QY 493 TTCCAGGGTGCAGGATCAATTACTGGCCAAAGGAGGTTGCCTATGGCTGGATTACTATC 552  
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QY 481 AACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGTGGTTCAGCATAGTCCCATATGAA 540  
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QY 553 AACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGTGGTTCAGCATAGTCCCATATGAA 612  
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QY 541 ACCAATAATCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGGGAGCCCTCTACACAAGTCACT 600  
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QY 613 ACCAATAATCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGGGAGCCCTCTACACAAGTCACT 672  
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QY 601 TTTGTACCCCAAAAACAGACTATCGAGTCCCGAGATAATGCTCTGCAATTTGCGCTCTAT 660  
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QY 673 TTTGTACCCCAAAAACAGACTATCGAGTCCCGAGATAATGCTCTGCAATTTGCGCTCTAT 732  
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QY 661 GCGAAGGACTACAATGCTCTACACATAGCTTCTTGTGCTATGGGAAGGATCAGGCATC 720  
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QY 721 TGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAAATGAAATTTCTCAGGGAGCCCATGC 780  
DB |||||||





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Db	313	ATTTAC	CTGACT	GTATTC	CATGGAA	GAGCTAG	GGAAGT	GTATTC	CAAGGT	CCCCAG	CAAA	372	
Qy	301	GAGAC	ACCCGT	TTACT	CTGGAG	CCACGG	CAGCAT	CGGTG	CTCAG	GTGAA	AGT	360	
Db	373	GAGAC	ACCCGT	TTACT	CTGGAG	CCACGG	CAGCAT	CGGTG	CTCAG	GTGAA	AGT	432	
Qy	361	GAGTT	GCCAC	AAGGGT	TTCTGG	ATGTGG	GAGGAG	CCCTC	ACAC	TAACCT	TTTGAC	420	
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Qy	1201	CTTC	CTG	CAAG	GC	TATAT	TTTAC	AGCT	GATTTCT	GGGAG	CACAT	1260	
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Qy	1321	CCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACTAA	1365
Db	1393	CCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACTAA	1437
RESULT 5			
AAD00209			
ID	AAD00209	standard; DNA; 1464 BP.	
XX AC	AAD00209;		
XX XX	17-AUG-2000	(first entry)	
XX XX	Human soluble CD39 fusion DNA construct, pIL2LFlagSolCD39.		
XX KW	Soluble CD39; solCD39; human; apyrase activity; platelet activation;		
XX KW	unstable angina; myocardial infarction; stroke; coronary artery disease;		
XX KW	atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;		
XX KW	platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;		
XX KW	coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;		
XX KW	thrombus formation; occlusion; stenosis; restenosis; angiogenesis;		
XX KW	antitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;		
XX KW	cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.		
OS OS	Homo sapiens.		
OS OS	Synthetic.		
FH FT	Key	Location/Qualifiers	
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FT FT	1. .72	/tag= b	
FT FT	/note=	c	"Mature human interleukin 2 N-terminal end"
FT FT	73. .108	/product=	d
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FT FT	/note=	g	"Coding region of human soluble CD39 (solCD39)"
XX PN	W0200023459-A1.		
XX XX	27-APR-2000.		
XX XX	13-OCT-1999;	99WO-US022955.	
XX PR	16-OCT-1998;	98US-0104585P.	
XX PR	06-NOV-1998;	98US-0107466P.	
XX PR	13-AUG-1999;	99US-0149010P.	
XX PA	(IMMV ) IMMUNEX CORP.		
XX PI	Maliszewski CR, Gayle RB, Price VL, Gimpel SD;		
XX DR	WPI; 2000-339644/29.		
DR DR	P-PSDB; AAY70921.		
PT PT	New soluble CD39 polypeptides having apyrase activity, useful for		
PT PT	inhibiting angiogenesis and treating unstable angina, myocardial		
PT PT	infarction, stroke, coronary artery disease or injury.		
XX PS	Example 9; Page 107-109; 122pp; English.		
XX CC	The present DNA sequence is a fusion construct pIL2LFlagSolCD39,		
CC CC	comprising the leader peptide of human interleukin 2 (hIL2), 12 amino		

CC acids from the mature N-terminus of hIL2, a linker, FLAG tag sequence and  
CC soluble CD39 (solCD39) coding region, that has apyrase activity. This  
CC produces high levels of solCD39 expression and activity in the  
CC transfected cells. Soluble CD39 is constructed by removing the N- and C-  
CC terminal transmembrane domains. It retains the capacity to metabolize ATP  
CC and ADP at relevant concentrations and the ability to block and reverse  
CC ADP-induced platelet activation and recruitment, including platelet  
CC aggregation. Soluble CD39 polypeptides are useful for inhibiting  
CC angiogenesis. It is useful for the treatment of unstable angina,  
CC myocardial infarction, stroke, coronary artery disease or injury,  
CC atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism,  
CC platelet-associated ischaemic disorders including lung, coronary and  
CC cerebral ischaemia, thrombotic disorders including coronary, peripheral  
CC and cerebral artery thrombosis, intracardiac and venous thrombosis,  
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and  
CC transient ischaemic attack. Soluble CD39 is also useful for preventing  
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or  
CC restenosis of blood vessels or stroke  
XX  
SQ Sequence 1464 BP; 424 A; 340 C; 342 G; 358 T; 0 U; 0 Other;

Query Match 97.3%; Score 1328; DB 3; Length 1464;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1334; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 11 CAAGTCTTACAAGAAACACACAGCTAACTAGTTCAACCCAGAACAAAGCAATGCCAGAAA 70  
DB 110 CTAGTTCAGGAGACTACAAGATGACGATGACAAAACCCAGAACAAAGCAATGCCAGAAA 169  
QY 71 AGTTTAAGTATGGGATTGTGCGGATGGGATGCGGGTCTTCTCACACAAGTTTATACATCTATA 130  
DB 170 AGCTTTAAGTATGGGATTGTGCGGATGGGATGCGGGTCTTCTCACACAAGTTTATACATCTATA 229  
QY 131 AGTGGCCAGCAGAAAAGAGAGATGACACAGCGGTGTGTCATCAAGTAGAAGAAATCAGGG 190  
DB 230 AGTGGCCAGCAGAAAAGAGAGATGACACAGCGGTGTGTCATCAAGTAGAAGAAATCAGGG 289  
QY 191 TTAAAGGTCTCGAATCTCAAAATTTGTTCAAGAAAGTAAATGAATAGGCATTTACCTGA 250  
DB 290 TTAAAGGTCTCGAATCTCAAAATTTGTTCAAGAAAGTAAATGAATAGGCATTTACCTGA 349  
QY 251 CTGATTGATGAAAGAGCTAGGAAGTGATTCAGAGTCCAGACCAAGACACCGG 310  
DB 350 CTGATTGATGAAAGAGCTAGGAAGTGATTCAGAGTCCAGACCAAGACACCGG 409  
QY 311 TTACTCTGGAGCCAGCGCAGCATGCGGTCTCTCAGGATGGAAGTGAAGATTGGCAG 370  
DB 410 TTACTCTGGAGCCAGCGCAGCATGCGGTCTCTCAGGATGGAAGTGAAGATTGGCAG 469  
QY 371 ACAGGGTTCTGGATGTGTGGAGAGAGCGCTCAGCAACTACCCCTTTTGACTTTCCAGGGTG 430  
DB 470 ACAGGGTTCTGGATGTGTGGAGAGAGCGCTCAGCAACTACCCCTTTTGACTTTCCAGGGTG 529  
QY 431 CCAGGATCACTACTGCCAAGAGAGGTGCGCTATGGCTGGATTAATCACTATCACTATCTGC 490  
DB 530 CCAGGATCACTACTGCCAAGAGAGGTGCGCTATGGCTGGATTAATCACTATCACTATCTGC 589  
QY 491 TGGGCAAAATTCAGTCAGAAAACAAGTGTTCAGCATAGTCCCATATGAAACCAATATC 649  
DB 590 TGGGCAAAATTCAGTCAGAAAACAAGTGTTCAGCATAGTCCCATATGAAACCAATATC 699  
QY 551 AGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCGCTCTACAAAGTCACTTTTGATACCCC 610  
DB 650 AGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCGCTCTACAAAGTCACTTTTGATACCCC 709  
QY 611 AAACACAGATATCAGTCCCGCCAGATATGCTCTGCAATTTGCGCTCTATGGCAAGGACT 670  
DB 710 AAACACAGATATCAGTCCCGCCAGATATGCTCTGCAATTTGCGCTCTATGGCAAGGACT 769  
QY 671 ACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACTCTGGCAGAAC 730  
DB 770 ACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACTCTGGCAGAAC 829

QY 731 TGGCCAAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCCATGCTTTTCATCTCTG 790  
DB 830 TGGCCAAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCCATGCTTTTCATCTCTG 889  
QY 791 GATATAAGAGGTAGTGAACGTAACTTTTACAAGACCCCTTGCACACAGAGATTG 850  
DB 890 GATATAAGAGGTAGTGAACGTAACTTTTACAAGACCCCTTGCACACAGAGATTG 949  
QY 851 AGATGACTCTTTCATTTCCAGCAGTATTGAAATCCAGGGTATTGGAACTATCAACAATGCC 910  
DB 950 AGATGACTCTTTCATTTCCAGCAGTATTGAAATCCAGGGTATTGGAACTATCAACAATGCC 1009  
QY 911 ATCAAGCATCTCGAGCTCTTCAACACAGTACTTGCCTTTACTCCAGTGTGCTTCA 970  
DB 1010 ATCAAGCATCTCGAGCTCTTCAACACAGTACTTGCCTTTACTCCAGTGTGCTTCA 1069  
QY 971 ATGGGATTTCTTGGCCACACTCCAGGGGGATTTTGGGGCATTTTCAGCTTTTACTTTG 1030  
DB 1070 ATGGGATTTCTTGGCCACACTCCAGGGGGATTTTGGGGCATTTTTCAGCTTTTACTTTG 1129  
QY 1031 TGATGAAGTCTTAAACTTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATCA 1090  
DB 1130 TGATGAAGTCTTAAACTTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATCA 1189  
QY 1091 TGAAGAAATCTCTGCTCAGCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGG 1150  
DB 1190 TGAAGAAATCTCTGCTCAGCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGG 1249  
QY 1151 AGAAGTACCTCAGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTGCAAG 1210  
DB 1250 AGAAGTACCTCAGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTGCAAG 1309  
QY 1211 GCTATCATTTTCAACAGCTGATTTCTGGGAGCACATCCATTTATTGGCAAGATCCAGGGCA 1270  
DB 1310 GCTATCATTTTCAACAGCTGATTTCTGGGAGCACATCCATTTATTGGCAAGATCCAGGGCA 1369  
QY 1271 CGCAGCGCGGTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTGAGC 1330  
DB 1370 CGCAGCGCGGTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTGAGC 1429  
QY 1331 AACCATTTGTCACACCTCTCTCCCACTCCACTAA 1365  
DB 1430 AACCATTTGTCACACCTCTCTCCCACTCCACTAA 1464  
RESULT 6  
AAD00204  
ID AAD00204 standard; DNA; 1464 BP.  
XX  
AC AAD00204;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Coding region of soluble CD39 expression plasmid.  
XX  
KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW peripheral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiatic;  
KW cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; solCD39 expression plasmid; se.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1464  
FT /\*tag= b  
FT /product= "SolCD39 expression plasmid protein"

FT	sig_peptide	1. .72	191	TTAAAGGTCCTGGAATCTCAAAATTTGTTGAGAAAGTAATGAAATAGGCAATTTACCTGA	250
FT		/*tag= a			
FT	mat_peptide	73. .108	290	TTAAAGGTCCTGGAATCTCAAAATTTGTTGAGAAAGTAATGAAATAGGCAATTTACCTGA	349
FT		/*tag= c			
FT		/product= "Mature human IL2"	251	CTGATTGCAATGMAAGAGCTAGGGAAGTGATTCCAAAGTCCACAGCTCCACAGCAACAAGACACCCG	310
FT		/note= "First N-terminal 12 amino acids"	350	CTGATTGCAATGMAAGAGCTAGGGAAGTGATTCCAAAGTCCACAGCTCCACAGCAACAAGACACCCG	409
FT	misc_feature	109. .120			
FT		/*tag= d	311	TTTACCTGGAGCCACGCGCAGGCATGCGGTTGCTCAGGATGGAAAGTGAAGAGTTGGCAG	370
FT	misc_feature	121. .144	410	TTTACCTGGAGCCACGCGCAGGCATGCGGTTGCTCAGGATGGAAAGTGAAGAGTTGGCAG	469
FT		/*tag= e			
FT		/*tag= "Flag tag"	371	ACAGGGTCTGGAATGTTGTTGAGAGGAGCCTCAGCAACTACACCTCTTTGACTTTCAGGGTG	430
FT	mat_peptide	145. .1461	470	ACAGGGTCTGGAATGTTGTTGAGAGGAGCCTCAGCAACTACACCTCTTTGACTTTCAGGGTG	529
FT		/*tag= f			
FT		/product= "Sol CD39"	431	CCAGGATCATTTACTTGGCCCAAGAGGAGTGCTTATGGCTGGATTACTATCAACTATCTGC	490
XX	WO200023094-A2.		530	CCAGGATCATTTACTTGGCCCAAGAGGAGTGCTTATGGCTGGATTACTATCAACTATCTGC	589
PN	27-APR-2000.				
XX			491	TGGGCAAAATTCAGTCAGAAAAACAAGGTGGTTTACGATAGTCCCATATGAAACCAATAATC	550
PF	13-OCT-1999;	99WO-US023641.	590	TGGGCAAAATTCAGTCAGAAAAACAAGGTGGTTTACGATAGTCCCATATGAAACCAATAATC	649
XX					
PR	16-OCT-1998;	98US-0104585P.	551	AGGAAACCTTTTGGAGCTTTGGACCTTGGGGAGGCTCTACACAAGTCACTTTTGTATCCCC	610
PR	06-NOV-1998;	98US-0107466P.	650	AGGAAACCTTTTGGAGCTTTGGACCTTGGGGAGGCTCTACACAAGTCACTTTTGTATCCCC	709
XX	13-AUG-1999;	99US-0149010P.			
XX	(IMMV ) IMMUNEX CORP.		611	AAAACAGACTATCGAGTCCCGCAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACT	670
PA	(CORR ) CORNELL RES FOUND INC.		710	AAAACAGACTATCGAGTCCCGCAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACT	769
XX	Maliszewski CR, Gayle RB, Marcus AJ;				
PI	WPI: 2000-339518/29.		671	ACAATGCTTACACACATAGCTTCTTTGTCTATGGAAAGGATCAGGCACTCTGGCAGAAAC	730
XX	P-PSDB; AAY70898.		770	ACAATGCTTACACACATAGCTTCTTTGTCTATGGAAAGGATCAGGCACTCTGGCAGAAAC	829
PT	Inhibiting platelet activation and recruitment, useful for treating a		731	TGGCCCAAGGACATTCAGGTTTGCAAGTAATGAAATTTCTCAGGAGCCCATGCTTTTCATCCTG	790
PT	mammal suffering from unstable angina, myocardial infarction, stroke,				
PT	coronary artery disease or injury, comprises administering soluble CD39		830	TGGCCCAAGGACATTCAGGTTTGCAAGTAATGAAATTTCTCAGGAGCCCATGCTTTTCATCCTG	889
PT	polypeptides.				
XX					
XX	Example 9; Page 107-109; 118pp; English.				
PS			791	GATATAAGAGGTAGTGAACGTAAAGTGAACCTTTTCAAGACCCCTCGACCAAGAGATTG	850
XX					
CC	The present sequence is the coding region of soluble CD39(solCD39)		890	GATATAAGAGGTAGTGAACGTAAAGTGAACCTTTTCAAGACCCCTCGACCAAGAGATTG	949
CC	expression plasmid. This was used for the transient expression of solCD39				
CC	protein in mammalian expression systems. SolCD39 is used in the treatment				
CC	of unstable angina, myocardial infarction, stroke, coronary artery				
CC	disease or injury, atherosclerosis, peripheral vascular occlusion,		851	AGATCACTCTTCCATTCACAGCAGTTTGAATTCAGGGTATTGGAACCTTATCAACAATGCC	910
CC	preclampsia, embolism, platelet-associated ischaemic disorder including				
CC	lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic		950	AGATCACTCTTCCATTCACAGCAGTTTGAATTCAGGGTATTGGAACCTTATCAACAATGCC	1009
CC	disorder including coronary artery thrombosis, cerebral artery				
CC	thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous		911	ATCAAAAGCATCTCGAGGCTCTTCAACACACAGTTACTGCGCTTACTCCAGTGGCTTCA	970
CC	thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),		1010	ATCAAAAGCATCTCGAGGCTCTTCAACACACAGTTACTGCGCTTACTCCAGTGGCTTCA	1069
CC	pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also				
CC	useful for preventing thrombus formation or reformation, occlusion,		971	ATGGGATTTTCTTGCCACCACTCCAGGGGGATTTTGGGGCATTTTTCAGCTTTTACCTTG	1030
CC	reocclusion, stenosis or restenosis of blood vessels or stroke				
CC			1070	ATGGGATTTTCTTGCCACCACTCCAGGGGGATTTTGGGGCATTTTTCAGCTTTTACCTTG	1129
XX					
SQ	Sequence 1464 BP; 424 A; 340 C; 342 G; 358 T; 0 U; 0 Other;				
			1031	TCATCAAGTTTTTAAACTTGCATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGA	1090
	Query Match 97.3%; Score 1328; DB 3; Length 1464;		1130	TCATCAAGTTTTTAAACTTGCATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGA	1189
	Best Local Similarity 98.5%; Pred. No. 0;				
	Matches 1334; Conservative 0; Mismatches 21; Indels 0; Gaps 0;				
Qy			1091	TCAAAAGATTTCTGTGCTCAGGCTTTGGGAGGAGATAAAAAACATCTTACGCTGGAGTAAAGG	1150
Db			1190	TGAAAAAGTTCTGTGCTCAGGCTTTGGGAGGAGATATAAAACATCTTACGCTGGAGTAAAGG	1249
Qy			1151	AGAAGTACCTGAGTGAATATCTGCTTTTCTGGTACTACTAATTTCTCTCCCTCTCTCGAAG	1210
Db			1250	AGAAGTACCTGAGTGAATATCTGCTTTTCTGGTACTACTAATTTCTCTCCCTCTCTCGAAG	1309
Qy			1211	GCTATCATTTTCACAGCTGAATTCCTGGGAGCATTCCATTTTCATTTGGCAAGAT	

QY 1271 GCGACGCGGCTGGACTTTGGGCTACATGCTGACCTGACCAACATGATCCAGCTGAGC 1330  
Db 1370 GCGACGCGGCTGGACTTTGGGCTACATGCTGACCTGACCAACATGATCCAGCTGAGC 1429  
QY 1331 AACCATTTGTCACACACTCTCTCCACTCCACCTAA 1365  
Db 1430 AACCATTTGTCACACACTCTCTCCACTCCACCTAA 1464

RESULT 7

AAD00205  
ID AAD00205 standard; cDNA; 1599 BP.

AC AAD00205;

XX 17-AUG-2000 (first entry)

XX Human soluble CD39 protein encoding cDNA.

XX Soluble CD39; human; apyrase activity; platelet activation; inhibitor;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;  
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;  
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;  
KW anti-anginal; cerebroprotective; anti-arteriosclerotic; anticoagulant;  
KW cardiac; vasotropic; thrombolytic; BS.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 67..1599

FT /tag= a

FT /product= "Human soluble CD39 protein"

FT /note= "Cell surface molecule"

XX WO200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US022955.

XX 16-OCT-1998; 98US-0104585P.

PR 06-NOV-1998; 98US-0107466P.

PR 13-AUG-1999; 99US-0149010P.

XX (IMMV) IMMUNEX CORP.

XX Malszewski CR, Gayle RB, Price VL, Gimpel SD;

XX WPI; 2000-339644/29.

DR P-PSDB; AAY70910.

XX New soluble CD39 polypeptides having apyrase activity, useful for  
PT inhibiting angiogenesis and treating unstable angina, myocardial  
PT infarction, stroke, coronary artery disease or injury.

XX Example 9; Page 85-87; 122pp; English.

XX The present sequence is the cDNA encoding the human soluble CD39 protein,  
CC a cell surface molecule, having apyrase activity. It is derived from a  
CC human B cell line cDNA library, referred to as MP-1. Soluble CD39 is  
CC constructed by removing the N- and C-terminal transmembrane domains. It  
CC retains the capacity to metabolise ATP and ADP at relevant concentrations  
CC and the ability to block and reverse ADP-induced platelet activation and  
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides  
CC are useful for inhibiting angiogenesis. It is useful for the treatment of  
CC unstable angina, myocardial infarction, stroke, coronary artery disease  
CC or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia,  
CC embolism, platelet-associated ischaemic disorders including lung,  
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,  
CC peripheral and cerebral artery thrombosis, intracardiac and venous  
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary

CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
CC stenosis or restenosis of blood vessels or stroke  
XX  
SQ Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;

Query Match 96.6%; Score 1319.2; DB 3; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 GTTCAACCCAGAACCAAGCATTTGCCAGAAAAAGCTTAAGTATGCGATTTGCTGGATGCCG 100  
Db 173 GGTGACCCAGAACCAAGCATTTGCCAGAAAAAGCTTAAGTATGCGATTTGCTGGATGCCG 232  
QY 101 GTTCTTCTCACACAAGTTTATATCATCTATTAAGTGGCCAGAGAAAGAGAAATGACACAG 160  
Db 233 GTTCTTCTCACACAAGTTTATATCATCTATTAAGTGGCCAGAGAAAGAGAAATGACACAG 292  
QY 161 GCGTGGTGCATCAAGTAGAAGATGACAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
Db 293 GCGTGGTGCATCAAGTAGAAGATGACAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 352  
QY 221 AGAAGTAATCAATAGATGCGATTTTACCTGACTGATTCGATGCAAGAGAGCTAGGAGTGA 280  
Db 353 AGAAAGTAATAGAAATAGGCACTTTACCTGACTGATTCGATGCAAGAGAGCTAGGAGTGA 412  
QY 281 TTCCAAGGTCCAGCAGCAACCAAGAGACACCCGTTTACTCTGGAGCCACGCGAGGATCGCGT 340  
Db 413 TTCCAAGGTCCAGCAGCAGCAGAGACACCCGTTTACTCTGGAGCCACGCGAGGATCGCGT 472  
QY 341 TGCTCAGGATGGAAAGTAGAAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGAGGCC 400  
Db 473 TGCTCAGGATGGAAAGTAGAAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGAGGCC 532  
QY 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTGGCCAGAGGAGGTG 460  
Db 533 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTGGCCAGAGGAGGTG 592  
QY 461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTGT 520  
Db 593 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTGT 652  
QY 521 TCAGCATAGTCCCATATGAAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
Db 653 TCAGCATAGTCCCATATGAAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 712  
QY 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCAGTCCCCAGATATG 640  
Db 713 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCAGTCCCCAGATATG 772  
QY 641 CTCTGCAATTTTGGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGCT 700  
Db 773 CTCTGCAATTTTGGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGCT 832  
QY 701 ATGGGAAGGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 760  
Db 833 ATGGGAAGGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 892  
QY 761 AAATTTCTCAGGGACCCATGCTTTTCATCTGATATATAGAAGGTAGTGAACGTAACTGACC 820  
Db 893 AAATTTCTCAGGGACCCATGCTTTTCATCTGATATATAGAAGGTAGTGAACGTAACTGACC 952  
QY 821 TTTTCAAGACCCCTGACCAAGAGATTGAGATGACTCTTCCATTCAGGAGATTTTGAAA 880  
Db 953 TTTTCAAGACCCCTGACCAAGAGATTGAGATGACTCTTCCATTCAGGAGATTTTGAAA 1012  
QY 881 TCCAGGATTTTGGAAACTATCAACAATGCCATCAAAAGCATCCTGGAGCTTTTCAACACCA 940  
Db 1013 TCCAGGATTTTGGAAACTATCAACAATGCCATCAAAAGCATCCTGGAGCTTTTCAACACCA 1072  
QY 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGATTTTCTTGGCCACACTCCAGGGGG 1000  
Db 1073 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGATTTTCTTGGCCACACTCCAGGGGG 1132

QY 1001 ATTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGCTTTTAAACTTTGACATCAGAGA 1060  
DB 1133 ATTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGCTTTTAAACTTTGACATCAGAGA 1192  
QY 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG 1120  
DB 1193 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG 1252  
QY 1121 AGATAAAAACATCTTACGCTTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1180  
DB 1253 AGATAAAAACATCTTACGCTTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1312  
QY 1181 GTRACCTACATCTCTCCCTCTCTCCAGAGGCTATCATTTTCAGCTGATTTCTGGGAGC 1240  
DB 1313 GTRACCTACATCTCTCCCTCTCTCCAGAGGCTATCATTTTCAGCTGATTTCTGGGAGC 1372  
QY 1241 ACATCATTTTCATTTGCAAGATCCAGGCGAGCGCGCTGGACTTTGGGGCTACATGC 1300  
DB 1373 ACATCATTTTCATTTGCAAGATCCAGGCGAGCGCGCTGGACTTTGGGGCTACATGC 1432  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGCCACCTCTCTCCCACTCCA 1360  
DB 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGCCACCTCTCTCCCACTCCA 1492  
QY 1361 CCTA 1364  
DB 1493 CCTA 1496

RESULT 8  
AAD00200  
ID AAD00200 standard; cDNA; 1599 BP.  
XX  
AC AAD00200;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Human soluble CD39 cDNA.  
KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombotic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antidiagonal; cardiant;  
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 67..1599  
FT /\*tag= a  
FT /product= "Soluble CD39 protein"  
XX  
PN WO200023094-A2.  
XX  
PD 27-APR-2000.  
XX  
PF 13-OCT-1999; 99WO-US023641.  
XX  
PR 16-OCT-1998; 98US-0104585P.  
XX  
PR 06-NOV-1998; 98US-0107466P.  
XX  
PR 13-AUG-1999; 99US-0149010P.  
XX  
XX (IMMV ) IMMUNEX CORP.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Maliszewski CR, Gayle RB, Marcus AJ;

Query Match 96.6%; Score 1319.2; DB 3; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGCGATTGTCTGGATGCGG 100  
DB 173 GGTTCACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGCGATTGTCTGGATGCGG 232  
QY 101 GTTCTTCTCACACAAGTTTATACATCTATTAAGTGGCCAGACAGAAAAGGAGATGACACAG 160  
DB 233 GTTCTTCTCACACAAGTTTATACATCTATTAAGTGGCCAGACAGAAAAGGAGATGACACAG 292  
QY 161 GGTGTGGTGCATCAAGTAGAAGAAATGAGGGTTAAAGGTCTCTGGAATCTCAAAATTTGTTTC 220  
DB 293 GGTGTGGTGCATCAAGTAGAAGAAATGAGGGTTAAAGGTCTCTGGAATCTCAAAATTTGTTTC 352  
QY 221 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTGTCATGGAAGAGAGTAGGGAAGTGA 280  
DB 353 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTGTCATGGAAGAGAGTAGGGAAGTGA 412  
QY 281 TTCCAAGGTCCAGCACCAGACAGACCCGTTTACTTGGAGCCACGGCAGGCATCGCGT 340  
DB 413 TTCCAAGGTCCAGCACCAGACAGACCCGTTTACTTGGAGCCACGGCAGGCATCGCGT 472  
QY 341 TGCTCAGGATGGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGGAGAGAGGCC 400  
DB 473 TGCTCAGGATGGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGGAGAGAGGCC 532  
QY 401 TCAGCAACTACCCCTTTTGACTTCCAGGGTGCAGAGATCATATTACTGCCCAAGAGGAGGTG 460  
DB 533 TCAGCAACTACCCCTTTTGACTTCCAGGGTGCAGAGATCATATTACTGCCCAAGAGGAGGTG 592  
QY 461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAATTTCACTCAGAAACAGAGGTGGT 520  
DB 593 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAATTTCACTCAGAAACAGAGGTGGT 652  
QY 521 TCAGCATAGTCCCATATGAACCAATTAATCAGAAACCTTTTGAGCTTTGGACCTTTGGGG 580  
DB 653 TCAGCATAGTCCCATATGAACCAATTAATCAGAAACCTTTTGAGCTTTGGACCTTTGGGG 712  
QY 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATTCGAGTCCCCCAGATAATG 640  
DB 713 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATTCGAGTCCCCCAGATAATG 772

XX  
DR WPI: 2000-339518/29.  
DR P-PSDB; AAY70887.  
XX  
PT Inhibiting platelet activation and recruitment, useful for treating a  
PT mammal suffering from unstable angina, myocardial infarction, stroke,  
PT coronary artery disease or injury, comprises administering soluble CD39  
PT polypeptides.  
XX  
PS Example 10; Page 85-87; 118pp; English.  
XX  
CC The present cDNA sequence encodes soluble CD39 having apyrase activity.  
CC This was derived from a cDNA library prepared from a human B cell line  
CC referred to as Mp-1. Soluble CD39 retains the capacity of wildtype CD39  
CC to metabolise ATP and ADP at physiologically relevant concentrations as  
CC well as the ability to block and reverse ADP-induced platelet activation  
CC and recruitment including platelet aggregation. This is used in the  
CC treatment of unstable angina, myocardial infarction, stroke, coronary  
CC artery disease or injury, atherosclerosis, peripheral vascular occlusion,  
CC preclampsia, embolism, platelet-associated ischaemic disorder including  
CC lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic  
CC disorder including coronary artery thrombosis, cerebral artery  
CC thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous  
CC thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),  
CC pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also  
CC useful for preventing thrombus formation or reformation, occlusion,  
CC reocclusion, stenosis or restenosis of blood vessels or stroke  
XX  
SQ Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;

QY 641 CTCGCAATTTGGCTCTATGGCAAGGACTACAAATGCTTACACACATAGCTTCTTGCT 700  
Db |||||  
QY 773 CTCGCAATTTGGCTCTATGGCAAGGACTACAAATGCTTACACACATAGCTTCTTGCT 832  
Db |||||  
QY 701 ATGGGAAGGATCAGGCACCTCTGSCAGAACTGSCCAAGGACATTCAGGTTGCAAGTAATG 760  
Db |||||  
QY 833 ATGGGAAGGATCAGGCACCTCTGSCAGAACTGSCCAAGGACATTCAGGTTGCAAGTAATG 892  
Db |||||  
QY 761 AAATCTCAGGGACCCATCTTTCATCTCGATATAGGAAGGTAGTGAACGTAAGTGACC 820  
Db |||||  
QY 893 AAATCTCAGGGACCCATCTTTCATCTCGATATAGGAAGGTAGTGAACGTAAGTGACC 952  
Db |||||  
QY 821 TTATACAGACCCCTGACCAAGAGATTTGAGATGACTCTTCATTTCCAGCATTTGAAA 880  
Db |||||  
QY 953 TTATACAGACCCCTGACCAAGAGATTTGAGATGACTCTTCATTTCCAGCATTTGAAA 1012  
Db |||||  
QY 881 TCCAGGATTTGGAACATATCAACATGCAATGCAATCAAGCATCTGGAGCTTTCACACCA 940  
Db |||||  
QY 1013 TCCAGGATTTGGAACATATCAACATGCAATGCAATCAAGCATCTGGAGCTTTCACACCA 1072  
Db |||||  
QY 941 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGCCACCATCCAGGGGG 1000  
Db |||||  
QY 1073 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGCCACCATCCAGGGGG 1132  
Db |||||  
QY 1001 ATTTTGGGCAATTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTGACATCAGAGA 1060  
Db |||||  
QY 1133 ATTTTGGGCAATTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTGACATCAGAGA 1192  
Db |||||  
QY 1061 AAGTCTCTCAGGAAAGGTGCTGAGATGATGAAAAGTTCTGCTCAGCCCTGGGAGG 1120  
Db |||||  
QY 1193 AAGTCTCTCAGGAAAGGTGCTGAGATGATGAAAAGTTCTGCTCAGCCCTGGGAGG 1252  
Db |||||  
QY 1121 AGATAAAACATCTTACGCTGGAGTAAGGAGAAGTACTGAGTGAATACTGCTTTTCTG 1180  
Db |||||  
QY 1253 AGATAAAACATCTTACGCTGGAGTAAGGAGAAGTACTGAGTGAATACTGCTTTTCTG 1312  
Db |||||  
QY 1181 GTACTACATTTCTCTCCCTCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTCGGAGC 1240  
Db |||||  
QY 1313 GTACTACATTTCTCTCCCTCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTCGGAGC 1372  
Db |||||  
QY 1241 ACATCCATTTCAATGGCAAGTCCAGGGCAGGAGCGCGCTGGACTTTGGGCTACATGC 1300  
Db |||||  
QY 1373 ACATCCATTTCAATGGCAAGTCCAGGGCAGGAGCGCGCTGGACTTTGGGCTACATGC 1432  
Db |||||  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGCAACACTCTCTCCCACTCCA 1360  
Db |||||  
QY 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGCAACACTCTCTCCCACTCCA 1492  
Db |||||

RESULT 9  
ADL24294  
ID ADL24294 standard; DNA; 1599 BP.  
XX  
AC ADL24294;  
XX

DT 03-JUN-2004 (first entry)  
XX  
DE Human CD39 coding sequence.

XX ds: gene; cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30;  
KW OX40; antagonist.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH 67..1599  
FT /\*tag= a  
FT /product= "CD39"

XX WO2004019866-A2.  
XX 11-MAR-2004.  
XX 21-AUG-2003; 2003WO-US026354.  
XX 28-AUG-2002; 2002US-0406418P.  
XX 12-AUG-2003; 2003US-0494457P.  
XX (IMMV ) IMMUNEX CORP.  
XX Burton PB, Deisher TA;  
XX WPI; 2004-239107/22.  
XX P-PSDB; ADL24295.  
XX Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a  
XX cardiovascular disease, e.g. chronic immune myocarditis, congestive heart  
XX failure, aneurysm, angina, embolism, restenosis, ischemia or  
XX thrombocytopenic purpura.  
XX Disclosure; Page 130-132; 135pp; English.  
XX The present invention relates to a method of treating cardiovascular  
XX disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,  
XX CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40  
XX antagonists are useful for treating cardiovascular disorders, e.g.  
XX (chronic immune) myocarditis, congestive heart failure, aneurysms,  
XX angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The  
XX present sequence is a coding sequence used in the exemplification of the  
XX invention.  
XX Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;  
Query Match 96.6%; Score 1319.2; DB 12; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATCGG 100  
Db |||||  
QY 173 GTTTACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATCGG 232  
Db |||||  
QY 101 GTTCTTCTCACACAAGTTTATACATCTATATAGTGGCCAGCAGAAAAGAGATGACACAG 160  
Db |||||  
QY 233 GTTCTTCTCACACAAGTTTATACATCTATATAGTGGCCAGCAGAAAAGAGATGACACAG 292  
Db |||||  
QY 161 GCGTGGTGCTCAAGTGAAGAAATGCAAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
Db |||||  
QY 293 GCGTGGTGCTCAAGTGAAGAAATGCAAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 352  
Db |||||  
QY 221 AGAAGTAAATGAATAGGCATTTTACCTGATTCATGGAAGAGCCTAGGGAAGTGA 280  
Db |||||  
QY 353 AGAAGTAAATGAATAGGCATTTTACCTGATTCATGGAAGAGCCTAGGGAAGTGA 412  
Db |||||  
QY 281 TTCCAAGGTCCTCAGCACCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT 340  
Db |||||  
QY 413 TTCCAAGGTCCTCAGCACCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT 472  
Db |||||  
QY 341 TGCTCAGGATGGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGCC 400  
Db |||||  
QY 473 TGCTCAGGATGGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGCC 532  
Db |||||  
QY 401 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTTGGCCACAGAGGAGTG 460  
Db |||||  
QY 533 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTTGGCCACAGAGGAGTG 592  
Db |||||  
QY 461 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 520  
Db |||||  
QY 593 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 652  
Db |||||  
QY 521 TCAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 580  
Db |||||



Db 653 TCAGCATAGTCCCATATGAACAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 712  
Qy 581 GAGCCTCTACAAAGTACATTTTGTACCCCAAAACCAGACTATCGAGTCCCGAGATAATG 640  
Db 713 GAGCCTCTACAAAGTACATTTTGTACCCCAAAACCAGACTATCGAGTCCCGAGATAATG 772  
Qy 641 CTCTGCAATTTCCCTCTATGGCAAGGACTTACAATGTCTACACATAGTCTTCTGTGCT 700  
Db 773 CTCTGCAATTTCCCTCTATGGCAAGGACTTACAATGTCTACACATAGTCTTCTGTGCT 832  
Qy 701 ATGGGAAGGATCAGGCACTCTGCGAGAAATGCGCAAGGACATTCAGGTTGCAAGTAATG 760  
Db 833 ATGGGAAGGATCAGGCACTCTGCGAGAAATGCGCAAGGACATTCAGGTTGCAAGTAATG 892  
Qy 761 AANTTCTCAGGACCCATGCTTTTCATCTCGGATATAAGAGGTAGTGAAGTGAAC 820  
Db 893 AANTTCTCAGGACCCATGCTTTTCATCTCGGATATAAGAGGTAGTGAAGTGAAC 952  
Qy 821 TTTTACAAGACCCCTCGCACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 880  
Db 953 TTTTACAAGACCCCTCGCACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1012  
Qy 881 TCAGGGTATTTGAAACTATCAACAATGCCATCAAGCATCTCGGAGCTTTCAACACCA 940  
Db 1013 TCAGGGTATTTGAAACTATCAACAATGCCATCAAGCATCTCGGAGCTTTCAACACCA 1072  
Qy 941 GTTACTGCCCTTACTCCAGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1000  
Db 1073 GTTACTGCCCTTACTCCAGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1132  
Qy 1001 ATTTTGGGGCATTTTTCAGCTTTTCTTCTGTGTGATGAAGTTTAACTTTGACATCAGAGA 1060  
Db 1133 ATTTTGGGGCATTTTTCAGCTTTTCTTCTGTGTGATGAAGTTTAACTTTGACATCAGAGA 1192  
Qy 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCTTTGGAGG 1120  
Db 1193 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCTTTGGAGG 1252  
Qy 1121 AGATAAACAATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1180  
Db 1253 AGATAAACAATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1312  
Qy 1181 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGCTGATTTCTCTGGAGC 1240  
Db 1313 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGCTGATTTCTCTGGAGC 1372  
Qy 1241 ACATCCATTTTCATTTGGCAAGATCCAGGCGACGACCGGCTGGAATTTGGGCTACATGC 1300  
Db 1373 ACATCCATTTTCATTTGGCAAGATCCAGGCGACGACCGGCTGGAATTTGGGCTACATGC 1432  
Qy 1301 TGAACCTGACCAACATGATCCGAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1360  
Db 1433 TGAACCTGACCAACATGATCCGAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1492  
Qy 1361 CCTA 1364  
Db 1493 CCTA 1496

RESULT 10  
AAA96069  
ID AAA96069 standard; DNA; 1704 BP.  
XX AC  
AC AAA96069;  
XX AC  
XX 29-JAN-2001 (first entry)  
XX Human ATP diphosphohydrolase coding sequence.  
XX Drug resistance; ATP gradient; chemotherapeutic; antibiotic; herbicide;  
KW human; ATP diphosphohydrolase; ds.  
XX  
XX Homo sapiens.

XX WO200052144-A1.  
PN 08-SEP-2000.  
XX 28-FEB-2000; 2000WO-US005315.  
PF 03-MAR-1999; 99US-00261825.  
XX (TEXA ) UNIV TEXAS.  
PA Thomas CE, Windsor JB, Roux SJ, Lloyd AM, Hurley L;  
PI WPI; 2000-587306/55.  
XX Increasing or decreasing drug resistance in target bacteria, yeast, plant  
PT or mammalian cells comprises altering ATP gradient across biological  
PT membrane of target cell.  
XX Claim 14; Page; 85pp; English.  
XX The present invention relates to a method for increasing or decreasing  
CC drug resistance in target bacteria, yeast, plant or mammalian cells by  
CC altering the ATP gradient across the biological membrane of the target  
CC cell. The method is useful for modulating drug resistance of cells. It is  
CC useful for increasing the sensitivity of cells to chemotherapeutic and  
CC antibiotic agents and increasing resistance to herbicides. The present  
CC sequence is human ATP diphosphohydrolase coding sequence. This sequence  
CC encodes was used in the present invention to modulate drug resistance.  
CC Note: The present sequence is not shown in the specification, but is  
CC referred to via its GenBank accession number  
XX Sequence 1704 BP; 468 A; 392 C; 403 G; 441 T; 0 U; 0 Other;  
SQ  
Query Match 96.6%; Score 1319.2; DB 3; Length 1704;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATCGG 100  
Db 137 GGTTCACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATCGG 196  
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAAATGACACAG 160  
Db 197 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAAATGACACAG 256  
Qy 161 GCGTGGTGATCAAGTAGAAGAAATGAGGTTAAAGGTTCTGGAATCTCAAAAATTTGTTTC 220  
Db 257 GCGTGGTGATCAAGTAGAAGAAATGAGGTTAAAGGTTCTGGAATCTCAAAAATTTGTTTC 316  
Qy 221 AGAAAGTAAATGAAATAGGCATTTACCTGACATTTGATGCAATGGAAGAGCTAGGGAAGTGA 280  
Db 317 AGAAAGTAAATGAAATAGGCATTTACCTGACATTTGATGCAATGGAAGAGCTAGGGAAGTGA 376  
Qy 281 TTTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCAGCGGATGCGGT 340  
Db 377 TTTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCAGCGGATGCGGT 436  
Qy 341 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGGAGCC 400  
Db 437 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGGAGCC 496  
Qy 401 TCAGCAACTACCCCTTTTGACTTTCCAGGGTGCCAGGATCATTTACTGCCCAAGAGGAGGTG 460  
Db 497 TCAGCAACTACCCCTTTTGACTTTCCAGGGTGCCAGGATCATTTACTGCCCAAGAGGAGGTG 556  
Qy 461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 520  
Db 557 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 616  
Qy 521 TCAGCATAGTCCCATATGAAACAATAATCAGGAAACCTTTTGAGCTTTGGACCTTTGGGG 580  
Db 617 TCAGCATAGTCCCATATGAAACAATAATCAGGAAACCTTTTGAGCTTTGGACCTTTGGGG 676





Qy	281	TTCCAGGTCCTCCAGCACCAGAGACACCCGTTTACCTGGAGGCCACGGCAGGATCGGCT	340
Db	377	TTCCAGGTCCTCCAGCACCAGAGACACCCGTTTACCTGGAGGCCACGGCAGGATCGGCT	436
Qy	341	TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTGGATGTGGTGGAGAGGCC	400
Db	437	TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTGGATGTGGTGGAGAGGCC	496
Qy	401	TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCATCTAGCCCAAGAGAGGTG	460
Db	497	TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCATCTAGCCCAAGAGAGGTG	556
Qy	461	CCTATGGCTGGATTACTATCAACTCTCTGTGGCAAAATTCAGTCAGAAAAACAAGTGGT	520
Db	557	CCTATGGCTGGATTACTATCAACTCTCTGTGGCAAAATTCAGTCAGAAAAACAAGTGGT	616
Qy	521	TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG	580
Db	617	TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG	676
Qy	581	GAGCCTCTACACAAGTCACCTTTGTATCCCAAAACAGACTATCGAGTCCCAAGATAATG	640
Db	677	GAGCCTCTACACAAGTCACCTTTGTATCCCAAAACAGACTATCGAGTCCCAAGATAATG	736
Qy	641	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTGTGCT	700
Db	737	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTGTGCT	796
Qy	701	ATGGGAAGGATCAGGCCTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG	760
Db	797	ATGGGAAGGATCAGGCCTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG	856
Qy	761	AAATTTCTCAGGAGCCCATGCTTTCATCTCGATATGAAGAGGTAGTGAAGTGAAC	820
Db	857	AAATTTCTCAGGAGCCCATGCTTTCATCTCGATATGAAGAGGTAGTGAAGTGAAC	916
Qy	821	TTTACAGACCCCTGACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAAA	880
Db	917	TTTACAGACCCCTGACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAAA	976
Qy	881	TCAGGAGTATTTGAAACTATCAACAATGCCATCAAGCATCTCGAGCTTCTCAACACCA	940
Db	977	TCAGGAGTATTTGAAACTATCAACAATGCCATCAAGCATCTCGAGCTTCTCAACACCA	1036
Qy	941	GTACTGCCCTTACTCCAGTGCCTTCAATGGGATTTTCTTGCACCACTCCAGGGG	1000
Db	1037	GTACTGCCCTTACTCCAGTGCCTTCAATGGGATTTTCTTGCACCACTCCAGGGG	1096
Qy	1001	ATTTTGGGGCATTTTCAAGCTTTTACTTTCTGTGATGAAGTTTAAACTTGACATCAGAG	1060
Db	1097	ATTTTGGGGCATTTTCAAGCTTTTACTTTCTGTGATGAAGTTTAAACTTGACATCAGAG	1156
Qy	1061	AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCTTGGAGG	1120
Db	1157	AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCTTGGAGG	1216
Qy	1121	AGATAAAAAATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATCTGTTTCTG	1180
Db	1217	AGATAAAAAATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATCTGTTTCTG	1276
Qy	1181	GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTTCTGGAGC	1240
Db	1277	GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTTCTGGAGC	1336
Qy	1241	ACATCCATTTTCAITGGCAAGATCCAGGCGCAGCGCGCTGGACTTTTGGGTACATGC	1300
Db	1337	ACATCCATTTTCAITGGCAAGATCCAGGCGCAGCGCGCTGGACTTTTGGGTACATGC	1396
Qy	1301	TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCCACCTCTCTCCCTCCA	1360
Db	1397	TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCCACCTCTCTCCCTCCA	1456
Qy	1361	CCTA 1364	

Db	1457	CCTA 1460	
RESULT 12			
AAT38516			
ID	AAT38516	standard; DNA; 1818 BP.	
XX	AC	AAT38516;	
XX	DT	29-DEC-1996 (first entry)	
XX	DE	Human lymphoid cell activation antigen CD39.	
XX	KW	ATP diphosphohydrolase; ATPdase; bovine aorta; pig pancreas; apyrase;	
KW	KW	CD39; lymphoid cell activation antigen; enzyme; platelet aggregation;	
KW	KW	thrombogenicity; anti-haemostatic; ss.	
OS	OS	Homo sapiens.	
PH	Key	Location/Qualifiers	
FT	CDS	68..1600	
FT		/*tag= a	
XX	PN	WO9632471-A2.	
PD	PD	17-OCT-1996.	
XX	PF	10-APR-1996; 96WO-CA000223.	
XX	PR	10-APR-1995; 95US-00419204.	
XX	PA	(UYSH ) UNIV SHERBROOKE.	
XX	PI	Beaudoin AR, Sevigny J;	
XX	DR	WPI; 1996-477122/47.	
XX	DR	P-PSDB; AAW04334.	
PT	PT	Isolated ATP di:phospho:hydrolase enzymes - have anti-haemostatic	
PT	PT	activity, useful for reducing platelet aggregation and thrombogenicity.	
PS	PS	Claim 18; Page 44-45; 60pp; English.	
XX	CC	The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine	
XX	CC	pancreatic (AAW04339) ATPdases have been partially sequenced. The	
XX	CC	sequences have been found to be highly homologous to a human lymphoid	
XX	CC	cell activation antigen designated CD39 (Maliszewski et al. (1994). J.	
XX	CC	Immunol.: 3574-3583). The complete sequences of the ATPdases types I and	
XX	CC	II have not been obtained yet. Assuming that the CD39 gene product is an	
XX	CC	ATPase type II, the use of CD39 in the reduction of platelet aggregation	
XX	CC	and of thrombogenicity may be contemplated, as well as a process of	
XX	CC	making ATPdases using the CD39 sequence (AAT38516)	
SQ	SQ	Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;	
Query Match	96.6%	Score 1319.2; DB 2; Length 1818;	
Best Local Similarity	99.8%	Pred. No. 0;	
Matches 1321; Conservative	0; Mismatches	3; Indels	0; Gaps
Qy	41	GTTCACCCAGAACAAAGCATTGCCAGAAACGTTAAGTATGGGATTTGCTGGATCGCG	100
Db	174	GTTGACCCAGAACAAAGCATTGCCAGAAACGTTAAGTATGGGATTTGCTGGATCGCG	233
Qy	101	GTTCCTTCTCACACAAGTTTATACATCTAATGTCGCCAGCAGAAAAAGGAGATGACACAG	160
Db	234	GTTCCTTCTCACACAAGTTTATACATCTAATGTCGCCAGCAGAAAAAGGAGATGACACAG	293
Qy	161	CGTGGTGCATCAAGTCAGAGAAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC	220
Db	294	CGTGGTGCATCAAGTCAGAGAAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC	353
Qy	221	AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTTGTCATGGAAAGAGCTAGGGAAGTGA	280

Db 354 AGAAAGTAATGAAATAGGACTTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGA 413  
Qy 281 TTCCAAAGTCCAGCACCAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCGATGCGGT 340  
Db 414 TTCCAAAGTCCAGCACCAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCGATGCGGT 473  
Qy 341 TGTCTAGGATGGAAGTGAAGATTGGCAGACAGAGTTCTGATGTGGTGGAGAGACC 400  
Db 474 TGTCTAGGATGGAAGTGAAGATTGGCAGACAGAGTTCTGATGTGGTGGAGAGAGCC 533  
Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGTTGCCAGGATCAATTATGCTGCCAAGAGAGGTG 460  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGTTGCCAGGATCAATTATGCTGCCAAGAGAGGTG 593  
Qy 461 CCTATGGCTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAACAAGTGTG 520  
Db 594 CCTATGGCTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAACAAGTGTG 553  
Qy 521 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 580  
Db 654 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 713  
Qy 581 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAAACAGACTATCAGTCCCCAGATAATG 640  
Db 714 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAAACAGACTATCAGTCCCCAGATAATG 773  
Qy 641 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACACATAGCTTTCTGTCT 700  
Db 774 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACACATAGCTTTCTGTCT 833  
Qy 701 ATGGAAGGATCAGGACTCTCGCAGAAACCTGCCAAGGACATTCAGGTTGCAAGTAATG 760  
Db 834 ATGGAAGGATCAGGACTCTCGCAGAAACCTGCCAAGGACATTCAGGTTGCAAGTAATG 893  
Qy 761 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACGTAGTGACC 820  
Db 894 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACGTAGTGACC 953  
Qy 821 TTTTCAAGACCCCTGCACCAAGAGATTGAGATGACTTCTTCATTCCAGCAGATTGAAA 880  
Db 954 TTTTCAAGACCCCTGCACCAAGAGATTGAGATGACTTCTTCATTCCAGCAGATTGAAA 1013  
Qy 881 TCCAGGGTATTGGAACATATCAACATGCCATCAAAAGCATCTGGAGCTTTTCAACACCA 940  
Db 1014 TCCAGGGTATTGGAACATATCAACATGCCATCAAAAGCATCTGGAGCTTTTCAACACCA 1073  
Qy 941 GTTACTGCGCTTACTCCAGTGCTGCTTCAATGGGATTTTCTGCGCACCATCTCCAGGGGG 1000  
Db 1074 GTTACTGCGCTTACTCCAGTGCTGCTTCAATGGGATTTTCTGCGCACCATCTCCAGGGGG 1133  
Qy 1001 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1060  
Db 1134 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1193  
Qy 1061 AAGTCTCTCAGAAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGGCTTTGGGAGG 1120  
Db 1194 AAGTCTCTCAGAAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGGCTTTGGGAGG 1253  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACGTCTTTTCTG 1180  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACGTCTTTTCTG 1313  
Qy 1181 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTTGGGAGC 1240  
Db 1314 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTTGGGAGC 1373  
Qy 1241 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGCGGTGGACTTTGGGCTACATGC 1300  
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGCGGTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAATGATCCAGCTGAGCAACCAATGTTCCACACTCTCTCTCCCACTCCA 1360

Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCACACTCTCTCTCCCACTCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497  
RESULT 13  
AAT33966  
ID AAT33966 standard; DNA; 1818 BP.  
XX AAT33966;  
AC AAT33966;  
XX 29-MAY-1997 (first entry)  
XX DNA coding for human CD39 protein.  
XX Human; lymphocyte activation marker; gene therapy;  
KW ATP diphosphohydrolase; transgenic animal; pig; porcine; graft; donor;  
KW transplantation; endothelial cell; prosthetic device;  
KW platelet aggregation; inhibition; intravascular; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 68.1600  
CDS /\*tag= a  
FT /EC number= "3.6.1.5"  
FT /note= "CD39 protein has ATP diphosphohydrolase activity"  
XX WO9630532-A1.  
XX 03-OCT-1996.  
XX 22-MAR-1996; 96WO-EP001270.  
XX 24-MAR-1995; 95US-00410371.  
PR 12-FEB-1996; 96US-00600383.  
XX (SANO ) SANDOZ LTD.  
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.  
XX Bach FH, Robson S;  
FI WPI; 1996-455377/45.  
DR P-PSDB; AAW04264.  
XX Gene therapy of inflammatory or immunological stimulation of platelet aggregation - using CD39 protein with ATP di:phospho:hydrolase activity, useful for preventing or alleviating thrombotic condition in mammalian subject.  
XX Claim 3; Page 38; 65pp; English.  
XX Non-human transgenic or somatic recombinant mammals, whose cells contain a heterologous DNA encoding a polypeptide (especially human CD39 protein) having ATP-diphosphohydrolase activity under cellular activating conditions is claimed. In particular the animal is a pig and its cells (or tissues or organs) can be used for transplantation. DNA coding for human CD39 is also useful for genetically modifying a mammalian cell to render it less susceptible to an inflammatory or immunological stimulus and platelet aggregation. The modified cells can be used to prevent or alleviate a thrombotic condition. The present sequence encodes human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-3584  
SQ Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;  
Query Match 96.6%; Score 1319.2; DB 2; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 41 GTTCAACCCAGCAAAAGCATTTGCCAGAAACGTTAAGATATGGGATTTGCTGATGCGG 100

Db 174 GGTGACCCAGAAACAAAGCATTCGCCAGAAAAACGTTAAGTATGGATTGTGCTGGATCGG 233  
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGATGACACAG 160  
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGATGACACAG 293  
Qy 161 GCCTGGTGCATCAAGTAGAAGAAATGACAGGTTAAAGGCTCTGGAATCTCAAAATTTGTTTC 220  
Db 294 GCCTGGTGCATCAAGTAGAAGAAATGACAGGTTAAAGGCTCTGGAATCTCAAAATTTGTTTC 353  
Qy 221 AGAAAGTAAATGAATAGGCAITTAACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 280  
Db 354 AGAAAGTAAATGAATAGGCAITTAACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 413  
Qy 281 TTCCAAGGTCACGACCAAGAGACACCCGTTTACCTTGGGAGCCACGGCAGGCAATCGGT 340  
Db 414 TTCCAAGGTCACGACCAAGAGACACCCGTTTACCTTGGGAGCCACGGCAGGCAATCGGT 473  
Qy 341 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGTTCTTGGATGTGGTGGAGAGGAGCC 400  
Db 474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGTTCTTGGATGTGGTGGAGAGGAGCC 533  
Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGGAAAGGTG 460  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGGAAAGGTG 593  
Qy 461 CCTATGGCTGGATTAATCAACTATCTGCTGGGCAATTCAGTCAAGAAACAAAGTGTGT 520  
Db 594 CCTATGGCTGGATTAATCAACTATCTGCTGGGCAATTCAGTCAAGAAACAAAGTGTGT 653  
Qy 521 TCAGCATAGTCCCATAGAAACCAATAATCAGAGAAACCTTTGAGCTTTGGACCTTGGGG 580  
Db 654 TCAGCATAGTCCCATAGAAACCAATAATCAGAGAAACCTTTGAGCTTTGGACCTTGGGG 713  
Qy 581 GAGCCTCTACACAAGTCACATTTTGTACCCCAAAACAGACATATCGAGTCCCCAGATAATG 640  
Db 714 GAGCCTCTACACAAGTCACATTTTGTACCCCAAAACAGACATATCGAGTCCCCAGATAATG 773  
Qy 641 CTCTGCAATTTGGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT 700  
Db 774 CTCTGCAATTTGGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT 833  
Qy 701 ATGGGAAGGATCAGGCACTCTGCAGAAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 760  
Db 834 ATGGGAAGGATCAGGCACTCTGCAGAAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 893  
Qy 761 AAATTTCTCAGGAGCCCATGCTTTTCATCTGGATATAAGAGGTAAGTGAACGTAAAGTGACC 820  
Db 894 AAATTTCTCAGGAGCCCATGCTTTTCATCTGGATATAAGAGGTAAGTGAACGTAAAGTGACC 953  
Qy 821 TTTACAAGACCCCTGACCAAGAGATTTGAGATGACTTTCATTTCCAGCAGTTTGAA 880  
Db 954 TTTACAAGACCCCTGACCAAGAGATTTGAGATGACTTTCATTTCCAGCAGTTTGAA 1013  
Qy 881 TCCAGGATTTGGAAACTATCAACAATGCCATCAAGAGCATCTCGGAGCTTCTCAACACCA 940  
Db 1014 TCCAGGATTTGGAAACTATCAACAATGCCATCAAGAGCATCTCGGAGCTTCTCAACACCA 1073  
Qy 941 GTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1000  
Db 1074 GTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1133  
Qy 1001 ATTTTGGGGATTTTACGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1060  
Db 1134 ATTTTGGGGATTTTACGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1193  
Qy 1061 AAGTCTCTCAGGAAAGGTCACATGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGAGG 1120  
Db 1194 AAGTCTCTCAGGAAAGGTCACATGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGAGG 1253  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTCTG 1180  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTCTG 1313

Qy 1181 GPACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGAGC 1240  
Db 1314 GPACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGAGC 1373  
Qy 1241 ACATCATTTTCATTTGGCAAGATCCAGGGCAGCGCCGGCTGGACTTTGGGCTACATGC 1300  
Db 1374 ACATCATTTTCATTTGGCAAGATCCAGGGCAGCGCCGGCTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAACATGATGCCAGCTGAGCAACCATTTGTCCACACTCTCTCTCCACTCCA 1360  
Db 1434 TGAACCTGACCAACATGATGCCAGCTGAGCAACCATTTGTCCACACTCTCTCTCCACTCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497

RESULT 14  
ADI32149  
ID ADI32149 standard; cDNA; 1818 BP.  
XX  
AC ADI32149;  
DT 17-JUN-2004 (first entry)  
XX  
Human cDNA #1475.  
DE  
XX  
KW Human; gene; ss; immunological response; immunopathological condition;  
Crohn's disease; asthma; ulcerative colitis; hyper eosinophilia;  
irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;  
acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;  
osteopathic; antiarthritic; antirheumatic; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US6607879-B1.  
XX  
PD 19-AUG-2003.  
XX  
PF 09-FEB-1998; 98US-00023655.  
XX  
PR 09-FEB-1998; 98US-00023655.  
XX  
PA (INCY-) INCYTE CORP.  
XX  
PI Cocks BG, Stuart SG, Seilhamer JJ;  
XX  
DR WPI; 2003-895307/82.  
XX  
A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.  
XX  
PS Claim 1; SEQ ID NO 1475; 50pp; English.  
XX  
CC The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detecting the hybridisation complexes and comparing the levels of the detected complexes in a non-diseased sample, where an altered level of the detected complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray can be used in

CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,  
CC ulcerative colitis, hyperesoinophilia, irritable bowel syndrome,  
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukemia, and in  
CC identifying agents for the treatment of the diseases. The microarray may  
CC also be used in drug discovery and development, toxicological and  
CC carcinogenicity studies, forensics or pharmacogenomics. The composition  
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or  
CC genomic fragments. This sequence represents a human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification but was obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

Query Match 96.6%; Score 1319.2; DB 11; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 GTTCAACCAGAACAAAGCATTTGCCAGAAAAGTTAAGTATGGGATTTGGTGGATGCGG 100  
DB 174 GGTGACCCAGAACAAAGCATTTGCCAGAAAAGCTTAAAGTATGGGATTTGGTGGATGCGG 233  
QY 101 GTTCTTCTCACACAGATTATACATCTATAAGTGGCCAGCAAAAGGAGATGACAG 160  
DB 234 GTTCTTCTCACACAGATTATACATCTATAAGTGGCCAGCAAAAGGAGATGACAG 293  
QY 161 GCGTGGTGCATCAAGTAGAAGATGACAGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTT 220  
DB 294 GCGTGGTGCATCAAGTAGAAGATGACAGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTT 353  
QY 221 AGAAGTAGAATGAATAGGATTTACCTGACTGATTTGATGCAAGAGATAGGGAAGTGA 280  
DB 354 AGAAGTAGAATGAATAGGATTTACCTGACTGATTTGATGCAAGAGATAGGGAAGTGA 413  
QY 281 TTCCAAGGTCCTCAGCAGCAAGAGACACCCGTTTACTCTGGAGCCAGCGAGCATGCGGT 340  
DB 414 TTCCAAGGTCCTCAGCAGCAAGAGACACCCGTTTACTCTGGAGCCAGCGAGCATGCGGT 473  
QY 341 TGCTCAGGATGAAAAGTAGTAAAGATTTGGCAGACAGAGGTTCTGGATGTGGTGGAGAGAGCC 400  
DB 474 TGCTCAGGATGAAAAGTAGTAAAGATTTGGCAGACAGAGGTTCTGGATGTGGTGGAGAGAGCC 533  
QY 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTGGCCAAAGGAAGGTG 460  
DB 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTGGCCAAAGGAAGGTG 593  
QY 461 CCTATGGCTGGATTTACTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAGGTGGT 520  
DB 594 CCTATGGCTGGATTTACTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAGGTGGT 653  
QY 521 TCAGCATAGTCCCATATGAAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
DB 654 TCAGCATAGTCCCATATGAAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTTGGGG 713  
QY 581 GAGCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCAGTATCCAGCAATAATG 640  
DB 714 GAGCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCAGTATCCAGCAATAATG 773  
QY 641 CTCTGCAATTTGGCTCTATGCGAGGACTACAAATGCTACACATAGCTTCTTGCT 700  
DB 774 CTCTGCAATTTGGCTCTATGCGAGGACTACAAATGCTACACATAGCTTCTTGCT 833  
QY 701 ATGGGAAGGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTCGAAGTAATG 760  
DB 834 ATGGGAAGGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTCGAAGTAATG 893  
QY 761 AAATTTCTCAGGACCCCATCTTTTCACTCTGGATATAAGAAGGTAGTGAACGTAAGTGACC 820  
DB 894 AAATTTCTCAGGACCCCATCTTTTCACTCTGGATATAAGAAGGTAGTGAACGTAAGTGACC 953  
QY 821 TTTACAAAGCCCCCTGCACCAAGAGATTTGATGACTCTTCCATTCAGCAGATTTGAAA 880  
DB 954 TTTACAAAGCCCCCTGCACCAAGAGATTTGATGACTCTTCCATTCAGCAGATTTGAAA 1013

QY 881 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACACCA 940  
DB 1014 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACACCA 1073  
QY 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTTCGCCACCATCCAGGGGG 1000  
DB 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTTCGCCACCATCCAGGGGG 1133  
QY 1001 ATTTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1060  
DB 1134 ATTTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1193  
QY 1061 AAGTCTCTCAGAAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCCTTGGGAGG 1120  
DB 1194 AAGTCTCTCAGAAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCCTTGGGAGG 1253  
QY 1121 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1180  
DB 1254 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1313  
QY 1181 GTACTCATTCTCTCCCTCTCTTCAAGGCTATCATTTTTCAGAGCTGATTCCTGGGAGC 1240  
DB 1314 GTACTCATTCTCTCCCTCTCTTCAAGGCTATCATTTTTCAGAGCTGATTCCTGGGAGC 1373  
QY 1241 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGAGCGGCTGGAGCTTTGGGCTACATGC 1300  
DB 1374 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGAGCGGCTGGAGCTTTGGGCTACATGC 1433  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTTCACACCTCTCTCCCACTCCA 1360  
DB 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTTCACACCTCTCTCCCACTCCA 1493  
QY 1361 CCTA 1364  
DB 1494 CCTA 1497  
RESULT 15  
ADK60414  
ID ADK60414 standard; DNA; 1818 BP.  
XX  
AC ADK60414;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Angiogenesis differentially expressed gene #61.  
XX  
KW ds; vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;  
KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;  
KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;  
KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis.  
XX  
OS Homo sapiens.  
XX  
PN FR2836687-A1.  
XX  
PD 05-SEP-2003.  
XX  
PF 11-APR-2002; 2002FR-00004546.  
XX  
PR 04-MAR-2002; 2002FR-00002717.  
XX  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
XX  
PI Colin S, Schneider C, Al Mahmood S;  
XX  
DR WPI: 2004-013912/02.  
XX  
PT P-PSDB; ADK60421.  
PT  
Compositions for diagnosing, prognosing and treating angiogenic disorders including tumor vascularization and heart disease, comprise nucleic acid

or polypeptide differentially expressed in angiogenesis.

Claim 2; SEQ ID NO 290; 424pp; French.

The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide sequence. The invention is used to diagnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is particularly tumor vascularization, a retinopathy, rheumatoid arthritis, Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis, endometriosis associated with neovascularization, restenosis due to angioplasty, overproduction of tissue due to cicatrization, a peripheral vascular disease, hypertension, vascular inflammation, Raynaud disease, aneurism, arterial restenosis, thrombophlebitis, ischemia, angina, myocardial infarction, chronic heart disease, cardiac congestion or macular degeneration due to age or osteoporosis. This sequence corresponds to a differentially expressed DNA used in the composition of the invention.

Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

Query Match 96.6%; Score 1319.2; DB 12; Length 1818;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

41 GTTCAACCCAGAACAAAGCATTCGCCAGAAACCTTAAGTATGGGATTTGCTGGATGCGG 100  
 174 GGTGACCCAGAACAAAGCATTCGCCAGAAACCTTAAGTATGGGATTTGCTGGATGCGG 233  
 101 GTTCTTCTCACAAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAAGGAGAATGACACAG 160  
 234 GTTCTTCTCACAAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAAGGAGAATGACACAG 293  
 161 GCCTGGTGCATCAAGTAGAGNATCGAGGTTAAAGTCTCGGAATCTCAAAATTTGTTTC 220  
 294 GCCTGGTGCATCAAGTAGAGNATCGAGGTTAAAGTCTCGGAATCTCAAAATTTGTTTC 353  
 221 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGGAAGAGCTAGGGAAGTGA 280  
 354 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGGAAGAGCTAGGGAAGTGA 413  
 281 TTCCAAAGGTCCCAGCACCAGAGACACCCCTTTTACTGGAGGCCACGGCAGGCATCGGTT 340  
 414 TTCCAAAGGTCCCAGCACCAGAGACACCCCTTTTACTGGAGGCCACGGCAGGCATCGGTT 473  
 341 TGCTCAGGATGGAAGTAGAGCTTGGCAGACAGGGTTCTGGATGTGTCGAGAGGAGCC 400  
 474 TGCTCAGGATGGAAGTAGAGCTTGGCAGACAGGGTTCTGGATGTGTCGAGAGGAGGCC 533  
 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGAGAGGTG 460  
 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGAGAGGTG 593  
 461 CCTATGGCTGGATTAATCAACTATCTGCTGGGCAAAATTCAGTCAAGAAAAAAGGTGTT 520  
 594 CCTATGGCTGGATTAATCAACTATCTGCTGGGCAAAATTCAGTCAAGAAAAAAGGTGTT 653  
 521 TCAGCATAGTCCCATATGAACCAATTAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 580  
 654 TCAGCATAGTCCCATATGAACCAATTAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 713  
 581 GAGCCTCTACACAAAGTCACTTTTGTATCCCAACCAAGAGCTATCGAGTCCCAAGATAATG 640  
 714 GAGCCTCTACACAAAGTCACTTTTGTATCCCAACCAAGAGCTATCGAGTCCCAAGATAATG 773  
 641 CTCTGCAATTTGCGCTCTATGGCAAGGACTATCAATGTCTACACATAGCTTCTGTGCT 700  
 774 CTCTGCAATTTGCGCTCTATGGCAAGGACTATCAATGTCTACACATAGCTTCTGTGCT 833

701 ATGGGAAGGATCAGGCACTCTGGCAGAAACCTGGCCAGGACATTCAGGTGTCAGATTAATG 760  
 834 ATGGGAAGGATCAGGCACTCTGGCAGAAACCTGGCCAGGACATTCAGGTGTCAGATTAATG 893  
 761 AAATTTCTCAGGGAACCATGCTTTTCATCTCTGGATATGAAGAGTAGTGAACGTAAAGTACC 820  
 894 AAATTTCTCAGGGAACCATGCTTTTCATCTCTGGATATGAAGAGTAGTGAACGTAAAGTACC 953  
 821 TTTTACAAGACCCCTGCAACAGAGATTTGAGTCACTCTTCCATTTCCAGCAGTTTGAAG 880  
 954 TTTTACAAGACCCCTGCAACAGAGATTTGAGTCACTCTTCCATTTCCAGCAGTTTGAAG 1013  
 881 TCCAGGGTATTGGAAATCTATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA 940  
 1014 TCCAGGGTATTGGAAATCTATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA 1073  
 941 GTTACTGCGCTTACTTCCAGAGTGTGCTTCAATGGGATTTTCTTGGCAACACTTCCAGGGGG 1000  
 1074 GTTACTGCGCTTACTTCCAGAGTGTGCTTCAATGGGATTTTCTTGGCAACACTTCCAGGGGG 1133  
 1001 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1060  
 1134 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1193  
 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGG 1120  
 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGG 1253  
 1121 AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAGATACCTGAGTGAATACTGCTTTTCTG 1180  
 1254 AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAGATACCTGAGTGAATACTGCTTTTCTG 1313  
 1181 GTACCTTACATTTCTCTCCCTTCTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGAGC 1240  
 1314 GTACCTTACATTTCTCTCCCTTCTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGAGC 1373  
 1241 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGAGCGGCTGGAGCTTTTGGGCTACATGC 1300  
 1374 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGAGCGGCTGGAGCTTTTGGGCTACATGC 1433  
 1301 TGAACCTGACCAACATGATFCCAGCTGAGCAACCAATTTGTTCACACCTCTCTCCCACTCCA 1360  
 1434 TGAACCTGACCAACATGATFCCAGCTGAGCAACCAATTTGTTCACACCTCTCTCCCACTCCA 1493  
 1361 CCTA 1364  
 1494 CCTA 1497

Search completed: September 21, 2005, 17:05:27

Job time : 791.776 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 16:26:16 ; Search time 4874.93 Seconds  
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**Title:** US-09-807-660C-5

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Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 190321344

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : EST:★

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1: gb_est1:★
2: gb_est2:★
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2: qb_enc:
3: qb_hlc: *
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4: gb\_est3:★

5: gb\_est4:★

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6: 9b_eat5:
7: 9b_eat6: *

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8: gb\_gss1: \*

9: gb\_gb2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description	
	Score	Match	Length				
1	1063.6	77.9	1760	3	CR617781	full-length	
2	940.6	68.9	984	5	BX436692	BX436692 Mus muscu	
3	863	63.2	2410	3	AK029512	AK029512 Mus muscu	
4	863	63.2	4198	3	AK030601	AK030601 Mus muscu	
5	812.4	59.5	861	5	BX371889	BX371889 Mus muscu	
6	743.4	54.5	3563	3	AK028625	AK028625 Mus muscu	
7	730.2	53.5	1014	1	AL553150	AL553150 AGSCOURT	
8	727	53.3	1066	5	BM906668	BM906668 AGSCOURT	
9	720.6	52.8	897	1	AL552123	AL552123 AL552123	
10	702.2	51.4	1025	5	BX402316	BX402316 BX402316	
11	697.6	51.1	1023	1	AL547722	AL547722 AL547722	
12	656.8	48.1	952	5	BX327984	BX327984 BX327984	
13	652.6	47.8	1061	5	BM925184	BM925184 AGSCOURT	
14	645.2	47.3	808	2	BF664417	BF664417 602146163	
15	624.2	45.7	673	6	CB553295	CB553295 WMS00076	
16	622.4	45.6	799	5	BX335123	BX335123 BX335123	
17	588.4	43.1	754	4	BI771056	BI771056 603059615	
18	584.8	42.8	608	2	AW965942	AW965942 EST378015	
19	584.2	42.8	820	4	BI822675	BI822675 603036008	
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21	561.2	41.1	656	5	BU947405	BU947405 1047411.Y	
22	561	41.1	1112	1	AL576332	AL576332 AL576332	
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24	520.2	38.1	884	5	BQ711179	BQ711179 AGSCOURT	



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RESULT 2
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LOCUS BX436692 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP003YK21
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX436692
VERSION BX436692.2 GI:47007879
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 984)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30779500.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5524.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdnafs=CS0CAP003AF11QPI&c=5524.f.

FEATURES
Location/Qualifiers
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 68.9%; Score 940.6; DB 5; Length 984;
Best Local Similarity 97.9%; Pred. No. 7,6e-267;
Matches 949; Conservative 12; Mismatches 7; Indels 1; Gaps 1;

QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATCGGATTTGTCTGGATCGCG 100
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QY 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAG 160
Db 77 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAG 136
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QY	161	GGTGGTGCATCAAGTAGAAGAAATCGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTC	220
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QY	221	AGAAAGTAATAAGAAATAGGCAATTTACCTGACCTGATTGCAATGAAAGAGCTAGGGAAGTGA	280
Db	197	AGAAAGTAATAAGAAATAGGCAATTTACCTGACCTGATTGCAATGAAAGAGCTAGGGAAGTGA	256
QY	281	TTTCAAGGTCCTCAGCACTCAAGAGACACCCGGTTTACCTGGAGCCACGGCAGGCATCGCGT	340
Db	257	TTTCAAGGTCCTCAGCACTCAAGAGACACCCGGTTTACCTGGAGCCACGGCAGGCATCGCGT	316
QY	341	TGCTCAGGATGAAAGTAGAAGATTGGCAGACAGAGGGTTCTGATGTGTTGGAGAGAGCC	400
Db	317	TGCTCAGGATGAAAGTAGAAGATTGGCAGACAGAGGGTTCTGATGTGTTGGAGAGAGAGCC	376
QY	401	TCAGCAACTACCCCTTTTGACTTTCAGGGTGCAGGATCATTTACTGSCCAAGAGGAAGTG	460
Db	377	TCAGCAACTACCCCTTTTGACTTTCAGGGTGCAGGATCATTTACTGSCCAAGAGGAAGTG	436
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Db	437	CCTATGGCTGGATTACTATCACTATCTGCTGGGCCAAATTCAGTCAGAAAAACAAGTGGT	496
QY	521	TCAGCATAGTCCCATATGAACCAATAATCAAGAAAACTTTGGAGCTTTGGACCTTTGGGG	580
Db	497	TCAGCATAGTCCCATATGAACCAATAATCAAGAAAACTTTGGAGCTTTGGACCTTTGGGG	556
QY	581	GAGCCTCTACACAGTCACTTTGTACCCCAAAACAGACATATCGAGTCCCAAGTAATG	640
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QY	701	ATGGGAAGGATCAGGCATCTTGGCGAGAACTGGCCCAAGCAATTCAGGTTGCAAGTAATG	760
Db	677	ATGGGAAGGATCAGGCATCTTGGCGAGAACTGGCCCAAGCAATTCAGGTTGCAAGTAATG	736
QY	761	AAATTTCTCAGGAGCCATGCTTTTCATCTCTGGATATAGAAAGGTAGTGAACGTAGTACC	820
Db	737	AAATTTCTCAGGAGCCATGCTTTTCATCTCTGGATATAGAAAGGTAGTGAACGTAGTACC	796
QY	821	TTTACAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTTCCATTTCCAGCAGTTTGAAA	880
Db	797	TTTACAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTTCCATTTCCAGCAGTTTGAAA	856
QY	881	TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCCTGGAGCTTTCAACACCA	940
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QY	941	GTTACTGCCCTTACTCCCAAGTGTGGCTTCAATGGGATTTCTTGGCACCACCTCCAGGGG	1000
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RESULT 3			
AK029512			
LOCUS			
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921511C05 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.		
ACCESSION	AK029512		
VERSION	AK029512.1 GI:26325463		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20493374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitesunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	6 (bases 1 to 2410)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kasugawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sugabe, Y., Tagami, M., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers
source	1. 2410 organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J"

Db	/db_xref="FANTOM_DB:4921511C05"																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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ORIGIN

Qy	1062	--AGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCGCTCGGAG	1119
Db	1241	GTCTCTCTCAGGAGAAATGACCGAGATACAAAAATTTTGTCTCAAAATCTTGGGAA	1300
Qy	1120	GAGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACCTGCTTTCT	1179
Db	1301	GAGACAAAGACATCTATCTCTTCAAGTAAAGGAGAAAGTACCTGAGTGAATACCTGCT	1360
Qy	1180	GGTACTCAATCT	1239
Db	1361	GGCGCTCATCATCT	1417
Qy	1240	CACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGCTGGAGTCTTGGGCTACATG	1299
Db	1418	CAGATTCAATTTATGGGCAAGATCAAGACAGAACCGGGTGGAGTCTTGGGCTACATG	1477
Qy	1300	CTGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCTCTCTCT	1359
Db	1478	CTGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCTCTCTCT	1537
Qy	1360	ACCTA 1364	
Db	1538	ACCTA 1542	

RESULT 4

AK030601	4198 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	Mus musculus adult male pituitary gland cDNA, RIKEN full-length			
DEFINITION	enriched library, clone:530437E10 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.			
ACCESSION	AK030601			
VERSION	AK030601.1	GI:26326590		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1 Carninci, P. and Hayashizaki, Y.			
AUTHORS	High-efficiency full-length cDNA cloning			
TITLE	Meth. Enzymol. 303, 19-44 (1999)			
JOURNAL	9279253			
MEDLINE	10349636			
PUBMED	2			
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			

**TITLE** Normalization and subtraction of cap-trapper-selected cDNAs to  
**JOURNAL** Prepare full-length cDNA libraries for rapid discovery of new genes  
**MEDLINE** Genome Res. 10 (10), 1617-1630 (2000)  
**PUBMED** 20499374  
**REFERENCE** 11042159  
**AUTHORS** 3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

**TITLE** RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
**JOURNAL** Genome Res. 10 (11), 1757-1771 (2000)  
**MEDLINE** 20530913  
**PUBMED** 11076861  
**REFERENCE** 4

**AUTHORS** The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
**TITLE** Functional annotation of a full-length mouse cDNA collection  
**JOURNAL** Nature 409, 685-690 (2001)  
**REFERENCE** 5

**AUTHORS** The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.

**TITLE** Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
**JOURNAL** Nature 420, 563-573 (2002)  
**REFERENCE** 6 (bases 1 to 4198)

**AUTHORS** Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.

**TITLE** Direct Submission  
**JOURNAL** Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

**COMMENT** cDNA library was prepared and sequenced in Mouse Genome  
cDNA library project of Genome Exploration Research Group in Riken  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

1. .4198

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="FANTOM DB:5330437E10"

/db\_xref="taxon:10090"

/clone="5330437E10"

/sex="male"

/tissue type="pituitary gland"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="adult"

93. .1625

**CDS**

/note="unnamed protein product; ectonucleoside  
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PFOGAKITQBEAGAGWITINLLGRFTQESWLSISDSQKQETFGALDGGAST  
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/note="putative"  
polyA\_site 4198  
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**ORIGIN**

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QY 46 ACCCAGAACAAAGCATTGCCAGAAACGTTAAAGTATGGGATTGTCTCGATCGCGGTTCT 105  
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QY 106 TCTCACACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAGGAGAAATGACACAGCGTG 165  
DB 264 TCTCACACAAACCTGTATCATCTACAAGTGGCGCGGAGGAGGAAATGACACAGCGGTG 323  
QY 166 GTGCATCAAGTAGAAGATGACAGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTCAGAAA 225  
DB 324 GTGCAGAGTTAGAGGAATGCAAGTGAAGAGTCTCTGGAATCTCAAAATTTGTTTCAGAAA 383  
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DB 384 ACAGATGAAATCGGTGGCTACCTGGCGAATGTCATGGAACCTGTCCACCGAACTGATACCA 443  
QY 286 AGTCCCGACCAAGAGACACCCGTTTACCTGGGAGCCAGCGAGGATGCGGTTGCTC 345  
DB 444 ACATCCAGCATACCCAGACTCTCTGTCTACCTGGGAGCCACAGCAGGATGCGGTTGCTT 503  
QY 346 AGGATGAAAGTGAAGAGTTGCGCAGACAGGTTCTGGAATGTTGTCAGAGAGAGCTCAGC 405  
DB 504 AGAATGGAAGCGAAACATATCGGCGAGACAGAGTCTGGCTGAGTGTCAACAGCCCTTAAG 563  
QY 406 AACTACCCCTTTGACTTTCAGGGTCCAGGATCATTTACTGGCCAGAGGAAGGTGCTTAT 465  
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QY 466 GGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAAGAAAACAGGTGTTTACG 525  
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QY 526 ATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGGGAGCC 585  
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QY 586 TCTACCAAGTCACTTTTGTACCCCAAAACAGAGTATCGAGTCCCAAGATAATGCTCTG 645  
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QY 646 CAATTTGCTCTATAGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGG 705  
DB 801 CAATTTGCTCTATAGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGG 860  
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QY 826 AAGACCCCTGACACCAAGAGATTGAGATGACTCTTCCATTCAGCAGATTGAAATCCAG 985
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QY 1006 GGGGCATTTTACGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAA- --- 1061
Db 1161 GGGGCGTTTCTGCTTCTACTTTTGTGATGATTTTAAAGAGGTAGCGAAACAGT 1220
QY 1062 --AGTCTCTCAGGAAAGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGAG 1119
Db 1221 GTCATCTCTCAGGAGAAATGACCGAGATAACAAAAATTTTGTCTCAAAATCTTGGGAA 1280
QY 1120 GAGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATCTGCTTTTCT 1179
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QY 1180 GGTACCTTACATCTCTCCCTCTCTCTCTC---CTGCAAGGCTATAACTTACACAGACAGCT 1239
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Db 1458 CTGAACCTGACCAACATGATCCAGCTGAGCAACCACTTGCCACACTCTCTCCCTCACTCC 1517
QY 1360 ACCTA 1364
Db 1518 ACCTA 1522

RESULT 5
BX371889/c
LOCUS
DEFINITION BX371889 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1073YD08 3-PRIME, mRNA sequence.
ACCESSION BX371889
VERSION BX371889.2 GI:46831287
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30456065.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5524.f
For more information about this cluster, see
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http://www.genoscope.cns.fr/cdna?s=CS0BAI027ZA08_CS02553_1&c=5524.f
FEATURES
source Location/Qualifiers
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 59.5%; Score 812.4; DB 5; Length 861;
Best Local Similarity 99.2%; Pred. No. 7.3e-229;
Matches 857; Conservative 0; Mismatches 3; Indels 4; Gaps 4;
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Db 801 CAGCAGAAAAGAGAAATGACACNAGCGTGTGTGCATCAAGTAGAAGAAATGCAGGGTTAAA 742
QY 196 GGTCTCTGGAATCTCAAAATTTTCTTTCAGAAAGTAAATGAAATAGGCAATTTACTGACTGAT 255
Db 741 GGTCTCTGGAATCTCANAAATTTTCTTTCAGAAAGTAAATGAAATAGGCAATTTACTGACTGAT 682
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 VERSION AK028625.1 GI:26324565  
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 1  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 2  
 Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 3563)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/.  
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VERSION AL553150.3 GI:45857920  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1014)

AUTHORS  
TITLE  
JOURNAL  
COMMENT

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31274964.

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5524.f

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DI073DB04QP1&c=5524.f.

FEATURES  
source

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REFERENCE 1 (bases 1 to 1066)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contract: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

ORIGIN
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VERSION AL552123.3 GI:45856912
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REFERENCE 1 (bases 1 to 897)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31273939.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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Db 788 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGCTGT 847
QY 701 ATGGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAG 747
Db 848 ATGGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAG 894
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## RESULT 11

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AL547722
LOCUS AL547722 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1017YB13 5-PRIME, mRNA sequence.
ACCESSION AL547722
VERSION AL547722.3 GI:45748162
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1023)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31269551.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5524.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0D1017CA07QPI&c=5524.f.
Location/Qualifiers
1..1023
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1017YB13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_libs="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
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## FEATURES source

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ORIGIN
Query Match 51.1%; Score 697.6; DB 1; Length 1023;
Best Local Similarity 98.6%; Pred. No. 8.4e-195;
Matches 697; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 41 GTTCAACCCAGAACAAAGCATTGGCCAGAAACGTTTAAGTATGGGATTGTGCTGGATGCGG 100
Db 188 GGTTCACCCAGAACAAAGCATTGGCCAGAAACGTTTAAGTATGGGATTGTGCTGGATGCGG 247
QY 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAAGAAAGAGAGATGACACAG 160
Db 248 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAAGAAAGAGAGATGACACAG 307
QY 161 GCGTGGTCATCAAGTGAAGAAATCCAGGTTTAAAGTCCCTGGATCTCAAAATTTGTTTC 220
Db 308 GCGTGGTCATCAAGTGAAGAAATCCAGGTTTAAAGTCCCTGGATCTCAAAATTTGTTTC 367
QY 221 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 280
Db 368 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 427
QY 281 TTCCAAGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGATGCGGT 340
Db 428 TTCCAAGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGATGCGGT 487
QY 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGAGAGAGCC 400
Db 488 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGAGAGAGCC 547
QY 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTGGCCAAAGAGAGGTG 460
Db 548 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTGGCCAAAGAGAGGTG 607
QY 461 CCTATGGCTGGATTAATCAATATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 520
Db 608 CCTATGGCTGGATTAATCAATATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 667
QY 521 TCAGCATAGTCCCATATGAACCAATATCAAGTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 580
Db 668 TCAGCATAGTCCCATATGAACCAATATCAAGTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 727
QY 581 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 640
Db 728 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 787
QY 641 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGCTGT 700
Db 788 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGCTGT 847
QY 701 ATGGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAG 747
Db 848 ATGGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAG 894
RESULT 12
BX327984 952 bp mRNA linear EST 07-APR-2004
BX327984 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1017YD08 5-PRIME, mRNA sequence.
ACCESSION BX327984
VERSION BX327984.1 GI:30332721
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 952)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5524.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS08BAG0362D06_CS03404_1&c=5524.f		
FEATURES	source	Location/Qualifiers	
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		/clone="CS001073YD08"	
		/tissue_type="PLACENTA COT 25-NORMALIZED"	
		/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"	
		/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN			
	Query Match	48.1%; Score 656.8; DB 5; Length 952;	
	Best Local Similarity	98.7%; Pred. No. 1e-182;	
	Matches	672; Conservative 0; Mismatches 8; Indels 1; Gaps 1;	
Qy	681	CACACATAGCTTCTTGCTGATGGGAGGATCAGGCACCTGCGCAGAACTGGCCCAAGGA	740
Db	23	CACACATAGCTTCTTGCTGATGGGAGGATCAGGCACCTGCGCAGAACTGGCCCAAGGA	82
Qy	741	CATTTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGCTTTTCATCTCGGATATAAGAA	800
Db	83	CATTTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGCTTTTCATCTCGGATATAAGAA	142
Qy	801	GGTAGTGAAGTAAGTGACCTTTACAGACCCCTGCGCAGAGATTTGAGATGACTCT	860
Db	143	GGTAGTGAAGTAAGTGACCTTTACAGACCCCTGCGCAGAGATTTGAGATGACTCT	202
Qy	861	TCCATTCCACGCTTTGAATCAGGATCAGGATTTGGAACATATCAACAATGCCATCAAGCAT	920
Db	203	TCCATTCCACGCTTTGAATCAGGATTTGGAACATATCAACAATGCCATCAAGCAT	262
Qy	921	CCTGGAGCTCTTCAACACCAAGTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTT	980
Db	263	CCTGGAGCTCTTCAACACCAAGTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTT	322
Qy	981	CTTGCCACCACTCCAGGGGATTTTGGGGATTTTCAGCTTTTACTTTGTGATGAAGTT	1040
Db	323	CTTGCCACCACTCCAGGGGATTTTGGGGATTTTTCAGCTTTTACTTTGTGATGAAGTT	382
Qy	1041	TTTAAACTTCACATCAGAGAACTCTCAGGAAAGGTCACATGATGATGAAAGTT	1100
Db	383	TTTAAACTTCACATCAGAGAACTCTCAGGAAAGGTCACATGATGATGAAAGTT	442
Qy	1101	CTGTGCTCAGCCTTGGGAGAGATAAAAAATCTTACCGCTGGAGTAAAGGAGAAGTACCT	1160
Db	443	CTGTGCTCAGCCTTGGGAGAGATAAAAAATCTTACCGCTGGAGTAAAGGAGAAGTACCT	502
Qy	1161	GAGTGAATACGTCTTTTGGTACCTACATCTCTCTCCCTCTCTGCAAGGCTATCATTT	1220
Db	503	GAGTGAATACGTCTTTTGGTACCTACATCTCTCTCCCTCTCTGCAAGGCTATCATTT	562
Qy	1221	CACAGCTGATCTCGGAGACATCCATTTTCATTGGCAGATCCAGGCGAGCCCGG	1280
Db	563	CACAGCTGATCTCGGAGACATCCATTTTCATTGGCAGATCCAGGCGAGCCCGG	622
Qy	1281	CTGGACTTTTGGGTACATGCTGTAACCTTGACCAACATGATCCCAAGTCAGCAACATTGTG	1340

Db	623	CTGGACTTTGGGCTACATGCTGAACCTGACCATGATCCACGATGAGCAACCATTTGT-	681
Qy	1341	CACACCTCTCTCCCACTCCAC	1361
Db	682	CACACCTGCTCTCCCACTCCAC	702
RESULT 13			
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LOCUS	AGENCOURT_6627603	NIH_MGC_122	Homo sapiens cDNA clone IMAGE:5762493
DEFINITION	5', mRNA sequence.		
ACCESSION	BM925184		
VERSION	BM925184.1	GI:19375563	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1061)		
AUTHORS	NIH-MGC http://mgs.nci.nih.gov/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12812 Row: m column: 22 High quality sequence start: 4 High quality sequence stop: 669. Location/Qualifiers 1..1061 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5762493" /lab_host="DH10B" /clone_lib="NIH MGC 122" /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."		
FEATURES	source		
	Query Match	47.8%; Score 652.6; DB 5; Length 1061;	
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	Matches	773; Conservative 0; Mismatches 49; Indels 11; Gaps 8;	
Qy	310	GTTTACCTCTGGGAGCCACGGCAGGCATGCGGTTGCTCAGGATCGAAAGTGAAGTTGGCA	369
Db	172	GTTTACCTCTGGGAGCCACAAAGCATTTGCCAGAAACGTTAAGGATGAAAGTGAAGTTGGCA	231
Qy	370	GACAGGTTCTGGATGTTGGTGAGAGGACCTCAGCACTACCCCTTTGACTTCAGGCT	429
Db	232	GACAGGTTCTGGATGTTGGTGAGAGGACCTCAGCACTACCCCTTTGACTTCAGGCT	291
Qy	430	GCAGGATCATTACTGGCCAAAGAGGAGTGCTTATGGCTGATTACTATCAACTATCTG	489
Db	292	GCAGGATCATTACTGGCCAAAGAGGAGTGCTTATGGCTGATTACTATCAACTATCTG	351
Qy	490	CTGGGCAATTCAGTCAGAAAAACAAGGTGGTTTCAGCATAGTCCCATATGAAACCAATAAT	549

Db 352 CTGGGCAATTCAGTCAGAAAAACAGGTGGTTCAGCATAGTCCCATATGAAACCAATAAT 411

Qy 550 CAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTGTACCC 609

Db 412 CAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTGTACCC 471

Qy 610 CAAAACAGACTATCAGATCCCGAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGAC 669

Db 472 CAAAACAGACTATCAGATCCCGAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGAC 531

Qy 670 TACAATGCTTACACACATAGCTTTCTGTGCTATGGGAAGGATCAGGACCTCTGGCAGAA 729

Db 532 TACAATGCTTACACACATAGCTTTCTGTGCTATGGGAAGGATCAGGACCTCTGGCAGAA 591

Qy 730 CTGGCCAAAGACATTCAGGTTGCAAGTAATGAAATTCCTCAGGACCCATGCTTTCAATCCT 789

Db 592 CTGGCCAAAGACATTCAGGTTGCAAGTAATGAAATTCCTCAGGACCCATGCTTTCAATCCT 651

Qy 790 GGNATATAAGAGTAGTGAACGTAAAGTACCTTTTACAAGACCCCTCGACCAAGATTT 849

Db 652 GGNATATAAGAGTAGTGAACGTAAAGTACCTTTTACAAGACCCCTCGACCAAGATTT 711

Qy 850 GAGATGACTCTTCATTCAGCAGAGTTTGAATCCAGGATTTGGAAACTATCAACAATGC 909

Db 712 GAGATGACTCTTCATTCAGCAGAGTTTGAATCCAGGATTTGGAAACTATCAACAATGC 771

Qy 910 CATCAAGCATCTCGAGCTCTTCAACACAGTTACTGCGCTTACTCCG-AGTGTGCCCT 968

Db 772 CATCAAGCATCTCGAGCTCTTCAACACAGTTACTGCGCTTACTCCGAGTGTGCCCT 831

Qy 969 CAATGGG--ATTTTCTTGCCACACATCCAGGGG--ATTTTGGGGCATTTTCAAG-TTTT 1023

Db 832 CAATGGGGATTTTCTTGGCCACACATCCAGGGGGATTTTGGGGCATTTTCAAGCTTTT 891

Qy 1024 TACTTTGTGATGAAGTTT--AACTTGACATCAGAG-AAAGTCTCTCAGGAAGG--T 1079

Db 892 TACTTTGGGATGGATTTTAAACCTTGACATCCGAGAAAGTCCCTCAGGAAAGGGTG 951

Qy 1080 GACTGAGATGATG-AAAAAGTTCTGTGCTCAGCTTGGGAGGAGATAAAAAACA 1131

Db 952 ACCTGGAATGATGAAAAAGTTCTGTGCTCAGCTTGGGAGGAGAGATAAA 1004

RESULT 14  
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LOCUS 602146163F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4309839 5',  
mRNA sequence.

ACCESSION BF664417.1 GI:11938222  
VERSION BF664417  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 808)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-romail.nih.gov](mailto:cgapbs-romail.nih.gov)  
Tissue Procurement: Louis M.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1183 row: n column: 16  
High quality sequence stop: 758.  
Location/Qualifiers  
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/organism="Homo sapiens"

FEATURES  
source

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/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
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for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 47.3%; Score 645.2; DB 2; Length 808;  
Best Local Similarity 98.7%; Pred. No. 2.6e-179;  
Matches 693; Conservative 0; Mismatches 3; Indels 6; Gaps 4;

Qy 604 GTACCCCAAAACACAGACTATCAGTCCCGAGATATGCTCTGCAATTTGCGCTCTATGGC 663

Db 2 GTACCCCAAAACACAGACTATCAGTCCCGAGATATGCTCTGCAATTTGCGCTCTATGGC 61

Qy 664 AAGGACTACAATGCTACACACATAGCTTTGTGCTATGGGAAGGATCAGGACCTCTCG 723

Db 62 AAGGACTACAATGCTACACACATAGCTTTGTGCTATGGGAAGGATCAGGACCTCTCG 121

Qy 724 CAGAACTGGCCAAAGCAATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTT 783

Db 122 CAGAACTGGCCAAAGCAATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTT 181

Qy 784 CATCTGATATAGAAGTAGTAACTAGTGACCTTTACAAGACCCCTGCAACCAAG 843

Db 182 CATCTGATATAGAAGTAGTAACTAGTGACCTTTACAAGACCCCTGCAACCAAG 241

Qy 844 AGATTGAGATGACTCTTCCATTCAGCAGATTTTGAATCCAGGGTATTGGAAACTATCAA 903

Db 242 AGATTGAGATGACTCTTCCATTCAGCAGATTTTGAATCCAGG--TATGGAACATATCAA 299

Qy 904 CAATGCCATAAAGCATCCTGGAGCTTTCAACACAGTTACTGCGCTTACTCCAGTGT 963

Db 300 CAATGCCATAAAGCATCCTGGAGCTTTCAACACAGTTACTGCGCTTACTCCAGTGT 359

Qy 964 GCCTTCATGGGATTTCTTCCGACCTCCAGGGGATTTTGGGGCATTTTCAAGCTTTT 1023

Db 360 GCCTTCATGGGATTTCTTCCGACCTCCAGGGG--ATTGGGGCATTTTCAAGCTTTT 417

Qy 1024 TACTTTGTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACT 1083

Db 418 TAC--TTGTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACT 476

Qy 1084 GAGATGATGAAAAAGTTCTGTGCTCAGCTTGGGAGGAGATAAAACATCTTACCTGGA 1143

Db 477 GAGATGATGAAAAAGTTCTGTGCTCAGCTTGGGAGGAGATAAAACATCTTACCTGGA 536

Qy 1144 GTAAGGAGAGTACCTGAGTGAATACCTGCTTTTCTGTGCTACCTCTCTCCCTCCTT 1203

Db 537 GTAAGGAGAGTACCTGAGTGAATACCTGCTTTTCTGTGCTACCTCTCTCCCTCCTT 596

Qy 1204 CTGCAAGGCTATCATTTTCAACAGTGTATCTTGGGAGGACATCCATTTTCTTGGCAAGATC 1263

Db 597 CTGCAAGGCTATCATTTTCAACAGTGTATCTTGGGAGGACATCCATTTTCA--TGGCAAGATC 655

Qy 1264 CAGGGCAGCAGCGCGCTGGACTTTTGGGCTTACATGCTGAAC 1305

Db 656 CAGGGCAGCAGCGCGCTGGACTTTTGGGCTTACATGCTGAAC 697

RESULT 15  
CB553295  
LOCUS

673 bp mRNA linear EST 01-JUN-2003

DEFINITION	MMSP0076_A03 MMSP Macaca mulatta cDNA, mRNA sequence.
ACCESSION	CB553295
VERSION	CB553295.1 GI:31302490
KEYWORDS	EST.
SOURCE	Macaca mulatta (rhesus monkey)
ORGANISM	Macaca mulatta
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
	Cercopithecoidea; Macaca.
REFERENCE	1 (bases 1 to 673)
AUTHORS	Katze, M.G., Bungarner, R., Korth, M., Feldman, R., Amjadi, M. and Holzman, T.
TITLE	Expressed sequence tags from Rhesus macaque spleen
JOURNAL	Unpublished (2002)
COMMENT	Contact: Holzman T
	Katze Lab
	University of Washington
	Box 358070, Seattle, WA 98195-8070, USA
	Tel: 206 732 6156
	Fax: 206 732 6055
	Email: ted@locke.ha.washington.edu
	Similar to GenBank entry S73813 S73813 CD39=lymphoid cell
	activation antigen [human, B lymphoblastoid cell line, MP-1, mRNA,
	1818 nt]. 4/1995
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	/sex="male"
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	/dev_stage="adult"
	/clone_lib="MMSP"
	/note="Organ: spleen"
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Best Local Similarity	98.4%; Pred. No. 4.2e-173;
Matches 662; Conservative	0; Mismatches 8; Indels 3; Gaps 3;
Qy	653 GCCTCTATGGCAAGGACTCAATGTCTACACATAGCTTCTTTGTG-CTATGGGAAGGAT 711
Db	
1	GCCTCTATGGCAAGGACTCAATGTCTACACATAGCTTCTTTGTGCTATGGGAAGGAT 60
Qy	712 CAGGCACTCTGGCAGAAACTGGCCAGGACATTCAGTTGCCAAGTAATGAAATTCACAG 771
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61	CAGGCACTCTGGCAGAAACTGGCCAGGACATTCAGTTGCCAAGTAATGAAATTCACAG 120
Qy	772 GACCCATGCTTTCATCTGGATATAGAAGGTAGTGAACGTAGTGACCTTTTACAAGACC 831
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121	GACCCATGCTTTCATCTGGATATAGAAGGTAGTGAACGTAGTGACCTTTTACAAGACC 180
Qy	832 CCCTGCACCAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAAATCCAGGGTATT 891
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181	CCCTGCACCAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAAATCCAGGGTATT 240
Qy	892 GGAAACTATCAAAATGCCATCAAAAGCATCCTGGAGCTCTTCAACACACAGTTACTGCCCT 951
Db	
241	GGAAACTATCAAAATGCCATCAAAAGCATCCTGGAGCTCTTCAACACACAGTTACTGCCCT 300
Qy	952 TACTCCAGTGCTTCAATGGGATTTTCTGCCACCTCCAGGGGATTTTGGGGCA 1011
Db	
301	TACTCCAGTGCTTCAATGGGATTTTCTGCCACCTCCAGGGGATTTTGGGGCA 360
Qy	1012 TTTTCAGCTTTTATCTTTGTGATGAAGTTTAAATTTGACATCAGAGAAAGTCTCTCAG 1071
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481	TCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACCTTTTCTGGTACCTACATT 540
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541	CTCTCCCTCTTCTGCAAGGCTATCATTTTTCACAGCTGATTCTCTGGAGCACATCCATT 600
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Qy	1310 CCAACATGATCCC 1322
Db	
661	CCAACATGATCCC 673
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Job time : 4882.93 secs	

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 16:29:41 ; Search time 244.55 Seconds  
(without alignments)  
9133.162 Million cell updates/sec

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Perfect score: 1365  
Sequence: 1 gcacctattcaagtgttac.....ctctctccactccacctaa 1365

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/prodata/1/ina/6C-COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1319.2	96.6	1818	3	US-08-930-921-2
2	1319.2	96.6	1818	4	US-09-023-655-1475
3	1319.2	96.6	1818	4	US-09-781-796C-2
4	463.2	33.9	871	4	US-09-949-016-2106
5	291.2	21.3	2782	4	US-09-949-016-5457
6	291.2	21.3	2797	3	US-09-240-639-3
7	291.2	21.3	2797	4	US-09-908-510A-3
8	291.2	21.3	2797	4	US-09-908-744B-3
9	291.2	21.3	2797	4	US-10-107-660-3
10	291.2	21.3	2797	4	US-10-107-576-3
11	291.2	21.3	2797	4	US-09-905-732B-3
12	291.2	21.3	2797	4	US-09-923-304-3
13	291.2	21.3	2797	4	US-09-949-016-1178
14	291.2	21.3	2797	4	US-09-905-743B-3
15	270.2	19.8	46885	4	US-09-949-016-13848
16	245.8	18.0	601	4	US-09-949-016-71601
17	220.8	16.2	1500	4	US-09-949-016-5688
18	167.8	12.3	364	4	US-09-513-999C-196
19	167.8	12.2	601	4	US-09-949-016-71600
20	140.4	10.3	601	4	US-09-949-016-71607
21	139.2	10.2	742	2	US-08-966-316-2
22	96.4	7.0	601	4	US-09-949-016-71597
23	69.4	5.1	9422	4	US-09-949-016-117430
24	69.4	5.1	45539	4	US-09-949-016-11920
25	69.4	5.1	45540	4	US-09-949-016-11799
26	53.2	3.9	1643	3	US-09-129-112-1
27	52.6	3.9	7218	1	US-08-232-463-14

c

ALIGNMENTS

RESULT 1

US-08-930-921-2  
; Sequence 2, Application US/08930921B  
; Patent No. 6287837  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; APPLICANT: SEVIGNY, Jean  
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN  
; CURRENT APPLICATION NUMBER: US/08/930,921B  
; CURRENT FILING DATE: 1998-01-02  
; EARLIER APPLICATION NUMBER: PCT/CA96/00223  
; EARLIER FILING DATE: 1996-04-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: unknown  
US-08-930-921-2

Query Match	96.6%	Score 1319.2;	DB 3;	Length 1818;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 1321;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	41	GTTCACCCAGCAACAAAGCATTCGCAGAAAACGTTAAGTATGGGATTCGCTGGATCGG	100	
Db	174	GGTTGACCCAGCAACAAAGCATTCGCAGAAAACGTTAAGTATGGGATTCGCTGGATCGG	233	
Qy	101	GTTCCTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAAGAAAGAGAGATGCACAG	160	
Db	234	GTTCCTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAAGAAAGAGAGATGCACAG	293	
Qy	161	CGCTGGTGATCAAGTAGAAGAAATGCAAGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTTC	220	
Db	294	CGCTGGTGATCAAGTAGAAGAAATGCAAGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTTC	353	
Qy	221	AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGGAAGAGTACAGGAGTGA	280	
Db	354	AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGGAAGAGTACAGGAGTGA	413	
Qy	281	TTCCAAAGTCCAGCACCAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCCGT	340	
Db	414	TTCCAAAGTCCAGCACCAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCCGT	473	
Qy	341	TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGGCC	400	



Db 474 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGCC 533  
Qy 401 TCAGCAACTACCCCTTTGACTTCAGGGTCCAGGATCATATTCTGGCCAAAGAGAGGTG 460  
Db 534 TCAGCAACTACCCCTTTGACTTCAGGGTCCAGGATCATATTCTGGCCAAAGAGAGGTG 593  
Qy 461 CCTATGGCTGGATTACTATCAACTATCTCTGGCCAAATTCAGTCAGAAAACAGGTGGT 520  
Db 594 CCTATGGCTGGATTACTATCAACTATCTCTGGCCAAATTCAGTCAGAAAACAGGTGGT 653  
Qy 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGG 580  
Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGG 713  
Qy 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 640  
Db 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 773  
Qy 641 CTCTGCAATTTCCGCTCTATGGCAAGGACTACATGCTCTACACATAGTCTTCTGTCT 700  
Db 774 CTCTGCAATTTCCGCTCTATGGCAAGGACTACATGCTCTACACATAGTCTTCTGTCT 833  
Qy 701 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 760  
Db 834 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893  
Qy 761 AAATTTCTCAGGGACCCATGCTTTTCACTCTGGATATGAAGAGGTAGTGAAGTGAAC 820  
Db 894 AAATTTCTCAGGGACCCATGCTTTTCACTCTGGATATGAAGAGGTAGTGAAGTGAAC 953  
Qy 821 TTTACAGACCCCTGCAACCAAGAGATTGAGATGACTCTTCATATCCAGCAGTTTGAA 880  
Db 954 TTTACAGACCCCTGCAACCAAGAGATTGAGATGACTCTTCATATCCAGCAGTTTGAA 1013  
Qy 881 TCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCTCGGAGCTCTTCAACACCA 940  
Db 1014 TCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCTCGGAGCTCTTCAACACCA 1073  
Qy 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGG 1000  
Db 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGG 1133  
Qy 1001 ATTTTGGGGCATTTTCACTTTTACTCTTGTGATGAAGTTTAAACTTGACATCAGAGA 1060  
Db 1134 ATTTTGGGGCATTTTCACTTTTACTCTTGTGATGAAGTTTAAACTTGACATCAGAGA 1193  
Qy 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGATTTCTGTGCTCAGCCTTTGGGAG 1120  
Db 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGATTTCTGTGCTCAGCCTTTGGGAG 1253  
Qy 1121 AGATAAAAAATCTTACGCTGGAGTAAAGAGAGTAACTCTGAGTGAATATCTGCTTTCTG 1180  
Db 1254 AGATAAAAAATCTTACGCTGGAGTAAAGAGAGTAACTCTGAGTGAATATCTGCTTTCTG 1313  
Qy 1181 GTACCTACATCTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGC 1240  
Db 1314 GTACCTACATCTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGC 1373  
Qy 1241 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCAGCGGCTGGACTTTGGGCTACATGC 1300  
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCAGCGGCTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1360  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497

US-09-023-655-1475  
; Sequence 1475, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1475:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g765255  
US-09-023-655-1475

Query Match 96.6%; Score 1319.2; DB 4; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATGCGG 100  
Db 174 GGTGACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATGCGG 233  
Qy 101 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGNATGACACAG 160  
Db 234 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGNATGACACAG 293  
Qy 161 GGTGTGTGCATCAAGTGAAGAAATGAGGTTTAAAGGTCCTCGAATCTCAAAATTTGTTTC 220  
Db 294 GGTGTGTGCATCAAGTGAAGAAATGAGGTTTAAAGGTCCTCGAATCTCAAAATTTGTTTC 353  
Qy 221 AGAAAGTAAATGAAATAGGCAATTTTACCTGACTGATTTGATGAGAAAGAGCTAGGGAAGTGA 280  
Db 354 AGAAAGTAAATGAAATAGGCAATTTTACCTGACTGATTTGATGAGAAAGAGCTAGGGAAGTGA 413  
Qy 281 TTCCAAGTCCAGACCAAGAGACACCCGTTTACCTGGAGGCCAGCGGATCGGT 340  
Db 414 TTCCAAGTCCAGACCAAGAGACACCCGTTTACCTGGAGGCCAGCGGATCGGT 473  
Qy 341 TGCTCAGGATGGAAGTGAAGAGTTTGGCAGACACAGGGTTCTGGATGTGGTGGAGGAGCC 400

Db 474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGGAGAGAGCC 533  
Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCCAAGGAAGGTG 460  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCCAAGGAAGGTG 593  
Qy 461 CCTATGGCTGGATTACTATCACTATCTCTGTGGCAAAATTCAGTCAGAAAAACAAGGTGT 520  
Db 594 CCTATGGCTGGATTACTATCACTATCTCTGTGGCAAAATTCAGTCAGAAAAACAAGGTGT 653  
Qy 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 580  
Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 713  
Qy 581 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACCCAGACTATCGAGTCCCAAGATAATG 640  
Db 714 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACCCAGACTATCGAGTCCCAAGATAATG 773  
Qy 641 CTCTGCAATTTGGCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTGTGCT 700  
Db 774 CTCTGCAATTTGGCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTGTGCT 833  
Qy 701 ATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCNAGGACATTCAGGTGCAAGTAATG 760  
Db 834 ATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCNAGGACATTCAGGTGCAAGTAATG 893  
Qy 761 AAATTTCTCAGGACCCCATCTTTCTCTGGATATAAGAAAGTGTGAACGTGAAGTACC 820  
Db 894 AAATTTCTCAGGACCCCATCTTTCTCTGGATATAAGAAAGTGTGAACGTGAAGTACC 953  
Qy 821 TTTTCAAGACCCCTGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 880  
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Qy 881 TCAGGGTATTGGAACACTATCAACATGCCATCAAGCATCTGGAGCTCTTCAACACCA 940  
Db 1014 TCAGGGTATTGGAACACTATCAACATGCCATCAAGCATCTGGAGCTCTTCAACACCA 1073  
Qy 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCCACCTCCAGGGGG 1000  
Db 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCCACCTCCAGGGGG 1133  
Qy 1001 ATTTTGGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTGACATCAGAGA 1060  
Db 1134 ATTTTGGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTGACATCAGAGA 1193  
Qy 1061 AGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCCTTGGGAGG 1120  
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Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1180  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1313  
Qy 1181 GTACCTACATCTCTCCCTCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGGGAGC 1240  
Db 1314 GTACCTACATCTCTCCCTCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGGGAGC 1373  
Qy 1241 ACATCCATTTTCTTGGCAAGATCCAGGGCAGGAGCCGGCTGGACTTTGGGCTACATGC 1300  
Db 1374 ACATCCATTTTCTTGGCAAGATCCAGGGCAGGAGCCGGCTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1360  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497

US-09-781-796C-2  
; Sequence 2, Application US/09781796C  
; Patent No. 6800284  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; APPLICANT: SEVIGNY, Jean  
; APPLICANT: BACH, Fritz H.  
; APPLICANT: ROBSON, Simon  
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: 920333.90019  
; CURRENT APPLICATION NUMBER: US/09/781,796C  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 08/419,204  
; PRIOR FILING DATE: 1995-04-10  
; PRIOR APPLICATION NUMBER: CA96/00223  
; PRIOR FILING DATE: 1996-04-10  
; PRIOR APPLICATION NUMBER: 08/930,921  
; PRIOR FILING DATE: 1998-02-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-781-796C-2

Query Match 96.6%; Score 1319.2; DB 4; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAACGTTAAGTATGGGATTTGCTGGATGCGG 100  
Db 174 GGTTCACCCAGACAAAGCATTTGCCAGAAAAACGTTAAGTATGGGATTTGCTGGATGCGG 233  
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGCCAGCAGAAAAAGAGAAATGACACAG 160  
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGCCAGCAGAAAAAGAGAAATGACACAG 293  
Qy 161 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAGGTCCTGGATCTCAAAATTTGTTTC 220  
Db 294 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAGGTCCTGGATCTCAAAATTTGTTTC 353  
Qy 221 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 280  
Db 354 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 413  
Qy 281 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGCATGCGGT 340  
Db 414 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGCATGCGGT 473  
Qy 341 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGGAGAGAGCC 400  
Db 474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGGAGAGAGCC 533  
Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCCAAGGAAGGTG 460  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCCAAGGAAGGTG 593  
Qy 461 CCTATGGCTGGATTACTATCACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 520  
Db 594 CCTATGGCTGGATTACTATCACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 653  
Qy 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 580  
Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 713  
Qy 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCCAGACTATCGAGTCCCAAGATAATG 640  
Db 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCCAGACTATCGAGTCCCAAGATAATG 773  
Qy 641 CTCTGCAATTTGCGCTCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTGTGCT 700

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Db 774 CTCTGCAATTTGGCTCTATGGCAAGGACTACAAATGCTCTACACATAGTCTTCTGTGCT 833
Qy 701 ATGGGAAGGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 760
Db 834 ATGGGAAGGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 893
Qy 761 AAATTCTCAGGGACCCAGTCTTTCATCTCGATATAGAAGGTAGTGAAGTAAAGTGACC 820
Db 894 AAATTCTCAGGGACCCAGTCTTTCATCTCGATATAGAAGGTAGTGAAGTAAAGTGACC 953
Qy 821 TTTTACAAGACCCCTCGCACCAAGAGATTTCAGATGACTTTCATTTCCAGCAGTTTGAAA 880
Db 954 TTTTACAAGACCCCTCGCACCAAGAGATTTCAGATGACTTTCATTTCCAGCAGTTTGAAA 1013
Qy 881 TCAGGGGTATTGGAACTATCAACAATGCCATCAAGCATCTCGGAGCTCTTCAACACCA 940
Db 1014 TCAGGGGTATTGGAACTATCAACAATGCCATCAAGCATCTCGGAGCTCTTCAACACCA 1073
Qy 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCCACCATCCAGGGGG 1000
Db 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCCACCATCCAGGGGG 1133
Qy 1001 ATTTTGGGGCAATTTTCAAGCTTTTCTTCTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1060
Db 1134 ATTTTGGGGCAATTTTCAAGCTTTTCTTCTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1193
Qy 1061 AAGTCTCTCAGGAAAGGTGACATGAGATGATGAAAAAGTTCTGTCTCAGCCCTTGGGAGG 1120
Db 1194 AAGTCTCTCAGGAAAGGTGACATGAGATGATGAAAAAGTTCTGTCTCAGCCCTTGGGAGG 1253
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATATCTGCTTTCTG 1180
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATATCTGCTTTCTG 1313
Qy 1181 GTACTACATTTCTCCTCCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTTCTCTGGAGC 1240
Db 1314 GTACTACATTTCTCCTCCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTTCTCTGGAGC 1373
Qy 1241 ACATCCATTTTCTTGGCAAGATCCAGGCGAGCGCGGCTGAGCTTTGGGCTACATGC 1300
Db 1374 ACATCCATTTTCTTGGCAAGATCCAGGCGAGCGCGGCTGAGCTTTGGGCTACATGC 1433
Qy 1301 TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1360
Db 1434 TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1493
Qy 1361 CCTA 1364
Db 1494 CCTA 1497

RESULT 4
US-09-949-016-2106
; Sequence 2106, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2106
; LENGTH: 871

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106

Query Match 33.9%; Score 463.2; DB 4; Length 871;
Best Local Similarity 99.4%; Pred. No. 2.3e-144;
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCCAGCAAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATGCCG 100
Db 198 GGTTCAGCCAGAACCAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATGCCG 257
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAAATGACACAG 160
Db 258 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAAATGACACAG 317
Qy 161 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTTAAAGGTCCTCGAAATCTCAAAAATTTGTTTC 220
Db 318 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTTAAAGGTCCTCGAAATCTCAAAAATTTGTTTC 377
Qy 221 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTCGATGAAAAGAGCTAGGGAATGA 280
Db 378 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTCGATGAAAAGAGCTAGGGAATGA 437
Qy 281 TTCCAAAGTCCAGACCAAGAGACACCCGTTTACCTGGAGCCACCGCAGGCGATCGCGT 340
Db 438 TTCCAAAGTCCAGACCAAGAGACACCCGTTTACCTGGAGCCACCGCAGGCGATCGCGT 497
Qy 341 TGCTCAGGATGAAAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGGAGAGGAGCC 400
Db 498 TGCTCAGGATGAAAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGGAGAGGAGCC 557
Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGAGTCAATTACTGCGCCAGAGGAGGTG 460
Db 558 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGAGTCAATTACTGCGCCAGAGGAGGTG 617
Qy 461 CCTATGGCTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCAGA 508
Db 618 CCTATGGCTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCAGA 665

RESULT 5
US-09-949-016-5457
; Sequence 5457, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5457
; LENGTH: 2782

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5457

Query Match 21.3%; Score 291; DB 4; Length 2782;
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

Qy 48 CCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTCGATGCGGGTTCTTC 107
Db 219 CAAGCAAGAGTCTCTCCCTCCAGGACTGAAGTATGTTGCTGATGCGGGTCTTC 278
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QY 108 TCACACAAAGTTTATACATCTATTAAGTGGCCAGAGAAAAGGAGAATGACACAGCGGTGGT 167
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QY 168 GCATCAAGTAGAAGATGAGGGTTAAAGTCTCGAATCTCAAAATTTGTTTCAGAAAGT 227
D 170 |||||
D 339 CAGTCAAACTCTCAAAATGTAGTGTGAAGGCTCTGAAATCTCCAGCTATGGAATAACCC 398
QY 228 AAATGAATAGGCATTTTACCTGACTGATTCATGGAAGAGCTAGGGAAGTGAATCCAAAG 287
D 290 |||||
D 399 CCAAGATGTCACAGAGCCTTTGAGGAGTGATGCAAAAAGTCAAGGGCAGGTTTCATC 458
QY 288 GTCCAGCACCAGAGACACCCCTTTTACCTGGAGCCACGGCAGGATCGGTGTCAG 347
D 290 |||||
D 459 CCACCTCCACGGATCACCCCTTCACTGGGAGCCACGGCTGGGATGCGCTTGCTGAG 518
QY 348 GATGGAAGTAGAGGTGGCAGACAGGGTTCTGGATGTTGGTGGAGAGGCTCAGCAA 407
D 350 |||||
D 519 GTTGCAAAATGAACACAGCAGCTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC 578
QY 408 CTACCCCTTTGACTTCCAGGGTCCAGGATCATTACTGGCCAAAGAGAGGTGCCTATGG 467
D 410 |||||
D 579 CCAGCCCTTTGACTTTAGGGTCTCAATCATTTCTGGCAGAGAAAGGGTATATGG 638
QY 468 CTGGATTACTATCACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAAGGTGTTTCAGCAT 527
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QY 588 TACACAAGTCACTTTTGTACCCCAAAACCAAGACTATCGAGTCCCGAGATAATGCTCTGCA 647
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QY 648 ATTTCCGCTCTATGGCAAGGACTACAAATGCTCTACACATAGTCTTCTGTGCTATGGGAA 707
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QY 708 GATCAGGACCTCTGCGAGAAACTGCGCAAGGACATTCAGGTTGCAAGTAATGAA--T 764
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D 767 |||||
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D 993 TGATAGCCTGTGACTGTGGACAGAGCCAGAAAGTTATACCCCAATGATGTATCATC 1052
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QY 1296 CATGCTGAACCTGACCAACATGATCCAGCTCAGCTAGCAACCATTTG 1338
D 1298 |||||
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RESULT 6
US-09-240-639-3
; Sequence 3, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischau, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(1669)
US-09-240-639-3

Query Match 21.3%; Score 291; DB 3; Length 2797;
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 48 CCAGAAACAAAGCATTTGCCAGAAAACGTTAAAGTATGGGATTTGCTGGATGCGGGTCTTTC 107
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D 220 CAAGCAAGAGGTCTCTCCCTCCAGGACTGAAAGTATGTTGCTGGATGCCGGGTCTTTC 279
QY 108 TCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAGGAGAATGACACAGGCTGT 167
D 110 |||||
D 280 AAGAACCAAGCTACTAGTGTATCAATGGCCAGCAGAAAAGAGAAATAATACCGAGTGT 339
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D 170 |||||
D 340 CAGTCAAACTTCAAAATGTAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAACCC 399
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D 460 CCACCTCAGCGATCCACCCCTTACCTGGAGCCACGGCTGGGATGCGCTTGTCTGAG 519
QY 348 GATGGAAGTGAAGATTTGGCAGACAGGGTTCTGGAATGTTGGTGGAGAGGAGCCTCAGCAA 407
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QY 408 CTACCCCTTTGACTTCCAGGGTGGCAGGATCAATTTCTGGCAGAGGAGGTCCTATGG 467
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D 640 ATGGATTACAGCCAACTAATTAATGGGAAATTTCTCTGGAGAGAAACCTGTGTGCAATGG 699
QY 528 AGTCCCATATGAACCAATATCAGGAAACCTTTTGGAGCTTTGGAGCTTTGGGGAGCCTC 587
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Db 1471 CATGCTCAGCTGACCAACAGATCCCAAGTCCAGCTGAAAGCCCTCTG 1513
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## RESULT 7

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US-09-908-510A-3
; Sequence 3, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischaufer, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(1669)
; OTHER INFORMATION:
US-09-908-510A-3
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Query Match 21.3%; Score 291; DB 4; Length 2797;
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;
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Qy 48 CCAGAACAAAGCAATTCGCCAGAAAACTTAAGTATGGATTTGCTCGATGCGGGTCTTCTTC 107
Db 220 CAAAGCAAGAGTCTCTCCCTCCAGGACTGAATATGTTATGCTCGATGCGGGTCTTCTTC 279
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Db 1471 CATGCTCAGCCTGACCAACAGATCCAGCTGAAAGCCCTCTG 1513

RESULT 8  
US-09-905-744B-3  
; Sequence 3, Application US/09905744B  
; Patent No. 6780410  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Friesch, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; TITLE OF INVENTION: ACIDS  
; FILE REFERENCE: 28110/36120A  
; CURRENT APPLICATION NUMBER: US/09/905,744B  
; PRIORITY FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIORITY FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-09-905-744B-3

Query Match 21.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 3.6e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 48 CCAGAACAAAGCATTTGCCAGAAACGTTAAGTATGGGATTTGCTGGATGCGGGTTCTTC 107  
Db 220 CAAGCAAGAGGTCCTCCCTCCAGGACTGAAGTATGGTATTTGCTGGATGCGGGTCTTC 279  
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RESULT 9  
US-10-107-660-3  
; Sequence 3, Application US/10107660  
; Patent No. 6780977  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna-Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
; FILE REFERENCE: 9598-066  
; CURRENT APPLICATION NUMBER: US/10/107,660  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: US/09/240,639  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
US-10-107-660-3  
Query Match 21.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 3.6e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;  
QY 48 CCAGAACAAAGCATTCGCCAGAAACCTTAAGTATGGATGTGCTGGATCGGGTTCTTC 107  
DB 220 CAAGCAAGAGGTCCTCCCTCCAGACTGAAGTATGTATGTGCTGGATGCGGGTCTTC 279  
QY 108 TCACACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAGCGCTGGT 167  
DB 280 AAGAACCAACAGTCTAGCTGTATCAATGGCCAGCAGAAAAGAGAAATATACCGAGTGT 339  
QY 168 GCATCAAGTAAAGATGACAGGGTTAAAGTCTCGGAATCTCAAAATTTGTTTCAGAAAGT 227  
DB 340 CAGTCAAAACCTTCAAAATGATGTGAAGGCTCTGGAATCTCCAGCTATGGAATTAACCC 399  
QY 228 AATGAATAGGATTTACCTGACTGTTGCATGGAAGAGCTAGGGAAGTATTCGAAG 287  
DB 400 CCAAGATGTCCCAGAGACCTTTGAGAGGTGTATGCAAAAAGTCAAGGGGAGGTTCCATC 459  
QY 288 GTCCCAGCAACAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATCGGTTGCTCAG 347  
DB 460 CCACCTCCAGGATCCACCCCAATTCACCTGGAGCCACGGCTGGATGGCTTGTCTGAG 519  
QY 348 GATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGAGAGAGAGCCCTCAGAA 407  
DB 520 GTTGCAAAATGAAACAGCAGCTAATGAAGTCTTGAAGCATCAAAAGCTACTTCAAGTC 579  
QY 408 CTACCCCTTTGACTTCAGGGTCCAGGATCATTAATCTGGCCAGAGAGAGGTCCTATGG 467  
DB 580 CCAGCCCTTTGACTTTAGGGGTGCTCAAAATCATTTCTGGGCAAGAAAGGGGTATATGG 639  
QY 468 CTGGATTACTATCAACTATCTGCTGGCAAAATTCAGTCAAAAAAAGGTGGTTTCAGCAT 527  
DB 640 ATGGATTACAGCCAACTAATTAATGGGAATTTCTGGAGAGAACTGTGGCAGATGTG 699  
QY 528 AGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTC 587  
DB 700 GGTGC-----ACCCGATGGAGTGAACCAACGGGTGCCCTGGAATAGGTGGTGGCTC 753  
QY 588 TACCAAGTCACTTTGTATCCCAACCAACAGACTATCGAGTCCCAGATAATGCTCTGCA 647  
DB 754 CACCAAAATATCTTCTGTGGCAGAGAGAGATGGATCTGAACACAGCGACATCATGCA 813  
QY 648 ATTTCGCTCTATGGCAAGGACTACATGTCTACACACATAGCTTCTTTGTGTATGGAA 707

DB 814 GGTTGCTCCCTGATGCTAGCTATACACGCTCTACACACACAGCTTCCAGTGTCTAGCGCG 873  
QY 708 GGATCAGGCACTCTGGCAGAACTGGCCAGAGACATTGAGGTGCAAGTAATGAAA---T 764  
DB 874 GAATGAGGCTGAGAAAGTTTCTGGCAATGCTCTCGAGAAATTCCTCTACCAAAACCA 933  
QY 765 TCTCAGGGAACCATGCTTTTCATCTCGGATATAGAAGGTAGTGAACGTAAAGTGACCTTTA 824  
DB 934 TCTCACCATCCCTGTACCTCGGATATAGCATCAGCTTCAACATGGGCCCATGTATT 993  
QY 825 CAAGACCCCTGCAC-----CAAGAGATTGAGATGACTCTTCCATCCAGAGTTTGA 878  
DB 994 TGATAGCCTGTGCACTGTGGACACAGAGGCCAGAAAGTTATAACCCCAATGATGTCAAC 1053  
QY 879 AATCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACAC 938  
DB 1054 TTTTGAAGGAACCTGGGACCCCATCTCTGTGAAGAGAAGGTGGCTTCCATATTTGACTT 1113  
QY 939 CAGTTTACTGCCCTTACTCCAG---TGTCCTTCAATGGGATTTTCTTTGCCACCACTCCA 995  
DB 1114 CAAAGCTTGCCATGATCAAGAAACCTGTCTTTTGTGGGTTTATCAGCCAAAGATTAA 1173  
QY 996 GGGGATTTGGGCAATTTTCAGCTTTTACCTTTGTGATGAAGTTTAAACTTGACATC 1055  
DB 1174 AGGGCAATTTGTGGCTTTTGCAGGATTTCTACTACACAGCCAGTGTCTTAAATCT---TTC 1230  
QY 1056 AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTGTCAGCCTTG 1115  
DB 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGGAAATTTCTGTCACAGAA 1290  
QY 1116 GGAGGAGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATATCTGCTT 1175  
DB 1291 GAGTCAGCTCCACCTGCTGCTCCCAATTTGATGAGGTATATGCCGCTCTTACTGCTT 1350  
QY 1176 TTCTGGTACTACATCT 1235  
DB 1351 CTCAGCAACTACATCTACCACTTGTGTTGTAACGGTTACAAATTCACAGAGGAGACTTG 1410  
QY 1236 GGAGCACATCCATTTTCATTGGCAAGATCCAGGGCAGCGCGGCTGCACTTTGGGCTA 1295  
DB 1411 GCCCCAAATACACTTTGAAAAAGAGTGGGGAATAGCAGCATAGCCTGTGCTCTTGGCTA 1470  
QY 1296 CATGCTGAACCTGACCACATGATCCAGCTGAGCAACCATTTG 1338  
DB 1471 CATGCTCAGCTGACCAACAGATCCAGCTGAAAGCCCTCTG 1513

RESULT 10  
US-10-107-576-3  
; Sequence 3, Application US/10107576  
; Patent No. 6783959  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; FILE REFERENCE: 28110/36120H  
; CURRENT APPLICATION NUMBER: US/10/107,576  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-10-107-576-3



Query Match									
Best Local Similarity 21.3%; Score 291; DB 4; Length 2797;									
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;									
QY	48	CCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGATTGTGCTGGATGCGGTTCTTC	107						
DB	220	CAAGCAAGAGTCTCCCTCCAGGACTGAAGTATGTTATGCTGGATGCCGGTCTTC	279						
QY	108	TCACACAAGTTTATACATCTATTAAGTGGCCAGAGAAAAGGAGAATGACACAGGCGTGT	167						
DB	280	AAGAACCAACAGTCTACGTGTATCAATGGCCAGCAGAAAAGAGAATAATACCGAGTGT	339						
QY	168	GCATCAAGTAGAAGATGAGGGTTAAAGTCTCGAATCTCAAAATTTGTTTCAGAAAT	227						
DB	340	CAGTCAAACTTCAAAATGAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAACCC	399						
QY	228	AAATGAAATAGGCATTTACTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGAATCCAAG	287						
DB	400	CCAGATGTCCCAGAGCCTTTGAGGAGTGTATGCANAAAGTCAAGGGCAGGTTCCATC	459						
QY	288	GTCCCAGACCAAGACACCCGTTTACTGCTGGAGCCACGGCATGCGGTTGCTCAG	347						
DB	460	CCACCTCCACGGATCACCCCATTCACCTGGAGCCACGGCTGGATGCGCTTGCTGAG	519						
QY	348	GATGNAAGTGAAGGTTGGCAGACAGGTTCTGATGTGGTGGAGAGGCTCAGCA	407						
DB	520	GTGCAAAATGAACACAGCAGCTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC	579						
QY	408	CTACCCCTTTGACTTCCAGGGTGCAGGATCAATCTGCGCAAGAGGAGGTGCCTATGG	467						
DB	580	CCAGCCCTTTGACTTTAGGGTGTCTCAATCAATTTCTGGCAAGAAAGAGGGGTATGG	639						
QY	468	CTGGAATTACTATCAACTACTCTGCGGCAAAATTCAGTCAGAAAAACAAGTGGTTCA	527						
DB	640	ATGGATTACAGCAACTATTTAATGGAAATTTCTCTGGAGAGAACCCTGTGSCACATGG	699						
QY	528	AGTCCCATATGAACCAATTAATCAGAAACCTTTGGAGCTTTGGAGCTTTGGGGAGCCTC	587						
DB	700	GGTG-----ACCCGCATGGAGTGGAAACCAACCGGTGCCCTGGACTAGGTGTGCCTC	753						
QY	588	TACACAAGTCACTTTTGTATACCCAAACCCAGACTATCGAGTCCCCAGATAATGCTGCA	647						
DB	754	CACCCAATATCTCTGTGGCAGGAGAGAGATGTGAATCTGAACACAGGACATCATGCA	813						
QY	648	ATTTCCCTCTTAGGCAAGGACTACAATGTCTTACACACATAGCTTCTTGTGCTATGGAA	707						
DB	814	GGTGTCCCTGTATGCTACGTATACACGCTCTACACACACACTCCAGTGTATGGCG	873						
QY	708	GGATCAGGCATCTGGCAGAACTGGCCAGGACATTCAGGTTGCAAGTAATGAAA---T	764						
DB	874	GAATGAGGCTGAGAGAAGTTTCTGGCAATGCTCTGCAGAAATCTCTACCAAAAAACA	933						
QY	765	TCTCAGGGACCATCTTTTCACTCTGGATATAAGAGGTAGTGAAGTAAAGTACCTTTA	824						
DB	934	TCTACCAATCTCTTACCCTCGGGATTATAGCATCAGCTTCAACATGGGCGATGTAT	993						
QY	825	CAAGACCCCTCGAC-----CAAGAGATTTGAGATGACTCTTCTCCATCTCCAGCAGTTGA	878						
DB	994	TGATAGCCTGTGCACTGTGGACACAGGCCAGAAAGTTATACCCCAATGATGTCATCAC	1053						
QY	879	AATCAGGGTATGGAACATATCAACAATGCCATCAAGCATCTCGGAGCTTCTCAACAC	938						
DB	1054	TTTTGAAGAACTGGGGACCATCTCTGTGTGAAGGAGAGGTGGCTTCCATATTTGACTT	1113						
QY	939	CAGTTACTGCCCTTACTCCCG--TGTCCTTCAATGGATTTTCTTGCCCACTCCA	995						
DB	1114	CAAGCTTGCCATGATCAAGAACTGTCTTTTGTATGGGTTTATCAGCCAAAGATPAA	1173						
QY	996	GGGGGATTTGGGGCATTTTCAAGCTTTTACTTTTGTGATGAAGTTTAAACTTGCATC	1055						
DB	1174	AGGGCAATTTGGGCTTTTGGAGGATTTCTACTACACAGCCAGTGTCTTAATCT---TTC	1230						
QY	1056	AGAGAAAGTCTCTCAGGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTG	1115						

DB	1231	AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTGGAATTTCTGCTCAGAAATG	1290						
QY	1116	GGAGCAGATAAAAACATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATACTGCTT	1175						
DB	1291	GAGTCAGCTCCACCTGCTGCTCCCAAAATTCATGAGGTATATGCCGCTCTTACTGCTT	1350						
QY	1176	TTCTGGTACCTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTCCTG	1235						
DB	1351	CTCAGCCAACTACATCTACCACTTGTGTTGAAACGTTTACAAATTCACAGAGGAGCTTG	1410						
QY	1236	GGAGCACATCCATTTTCATTTGGCAAGATCCAGGGCAGCAGCCGGCTGACACTTTGGGCTA	1295						
DB	1411	GCCCCAAAATACACTTTTGAAGAAAGTGGGGAATAGCAGCATAGCCTGCTCTCTTGGCTA	1470						
QY	1296	CATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTG	1338						
DB	1471	CATGCTAGCCTGACCAACCAACCATTTCCAGCTGGAAGCCCTCTG	1513						

RESULT 11

US-09-905-732B-3  
; Sequence 3, Application US/09905732B  
; Patent No. 6787328  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; FILE REFERENCE: 28110/36120B  
; CURRENT APPLICATION NUMBER: US/09/905,732B  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-09-905-732B-3

Query Match 21.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 3.6e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY	48	CCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGATTGTGCTGGATGCGGTTCTTC	107						
DB	220	CAAGCAAGAGTCTCCCTCCAGGACTGAAGTATGTTATGCTGGATGCCGGTCTTC	279						
QY	108	TCACACAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTGT	167						
DB	280	AAGAACCAACAGTCTACGTGTATCAATGGCCAGCAGAAAAGAGAATAATACCGAGTGT	339						
QY	168	GCATCAAGTAGAAGATGAGGGTTAAAGTCTCGAATCTCAAAATTTGTTTCAGAAAT	227						
DB	340	CAGTCAAACTTCAAAATGAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAACCC	399						
QY	228	AAATGAAATAGGCATTTTACTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGAATCCAAG	287						
DB	400	CCAGATGTCCCAGAGCCTTTGAGGAGTGTATGCANAAAGTCAAGGGCAGGTTCCATC	459						
QY	288	GTCCCAGACCAAGAGACACCCGTTTACTGCTGGAGCCACGGCATGCGGTTGCTCAG	347						
DB	460	CCACCTCCACGGATCCACCCCATTCACCTGGAGCCACGGCTGGATGCGCTTGCTGAG	519						
QY	348	GATGNAAGTGAAGGTTGGCAGACAGGTTCTGATGTGGTGGAGAGGACCTCAGCA	407						
DB	520	GTTCGAAAATGAACACAGCAGCTAATGAAGTCTTTGAAGAGCATCCAAAGCTACTTCAAGTC	579						



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QY      879  AATCCAGGATTTGGAAACTATCAACAATGCCATCAAGCATCTCGAGCTCTTCAACAC  938
Db      1054  TTTTGAAGGAATGGGGACCCATCTCTGTGTAAGGAAGGTGGCTTCCATATTTGACTT  1113
QY      939  CAGTTACTGCTTACTCCAG---TGTGCTTCAATGGATTTCTTCCACCACTCCA  995
Db      1114  CAAAGCTTGCCATGATCAAGAAACCTGTCTTTTGTATGGGTTTATCAGCCAAAGATTAA  1173
QY      996  GGGGATTTTGGGCAATTTTACGCTTTTACTTTGTGATGAAGTTTAAACTTGACATC  1055
Db      1174  AGGGCAATTTGGCTTTTTCAGGATTTCTACTACAGCCAGTGTCTTAAATCT---TTC  1230
QY      1056  AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTGCTCAGCCTTG  1115
Db      1231  AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACTTGAATTTCTGTCTCAGAAATTG  1290
QY      1116  GGAGGAGATAAAACATCTTACGCTGGAGTAAGGAGAAGTACCTGAGTGAATACTGCTT  1175
Db      1291  GAGTCAGCTCCCACTGCTCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT  1350
QY      1176  TTCTGTACTACATTTCTCTCTCTCTCTGCAAGGCTATCATTTACAGCTGATTCTCTG  1235
Db      1351  CTCAGCCAATCTACATCTACACTTGTGTGTAAGGTTACAAATTCACAGAGAGACTTG  1410
QY      1236  GGAGCACATCCATTTTCATTTGGCAAGATCCAGGCGACGCGGCTGGACTTTGGGGTA  1295
Db      1411  GCCCAAAATACACTTTGAAAAAGAGTGGGGAATAGCAGCATAGCTGTCTCTTGGCTA  1470
QY      1296  CATGCTGAACCTGACCAACATATCCAGCTCAGCTGAGCAACCAATTG  1338
Db      1471  CATGCTCAGCTGACCAACCATCCAGCTCCAGCTGAAAGCCCTCTG  1513
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## RESULT 13

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US-09-949-016-178
; Sequence 178, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-178
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Query Match      21.3%; Score 291; DB 4; Length 2797;
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;
```

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QY      48  CCAGAACAAAGCATTTCCAGAAACGTTTAAGTATCGGATTTGCTGGATGCGGGTCTTC  107
Db      220  CAAAGCAAGAGTCTCCCTCCAGGACTGAAGTATGGTATTTGCTGGATGCGGGTCTTC  279
QY      108  TCACACAAGTTTATACATCTATAAGTGGCCAGCAGAGAAAGGAGATGACAGAGGCTGGT  167
Db      280  AAGAACACAGCTTACGTGTATCAATGCGCAGCAGAGAAAGAGATATATACCGGAGTGGT  339
QY      168  GCATCAAGTAGAAGATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAGT  227
```

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Db      340  CAGTCAAAACCTTTCAAATGTAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAAACCC  399
QY      228  AATGAAATAGGCATTTACCTGACTGATTTCATGAAAGAGCTAGGAAAGTGAATTCGAAG  287
Db      400  CCNAGATGTCCAGAGCCTTTGAGGAGTGTATGCAAAAAGTCAAGGGCAGGTTCCATC  459
QY      288  GTCCAGCACCAAGAGACACCCGTTTAACTGGAGCCACGGCAGGATGCGGTGCTCAG  347
Db      460  CCACCTCCACGATCCACCCCATTTACCTGGAGCCACGGCTGGATGCGCTTGTCTGAG  519
QY      348  GATGAAAGTGAAGAGTTGGCAGACAGGGTCTCGATGTGGTGGAGAGGAGCCTCAGCAA  407
Db      520  GTTGAAAATGAACACAGCAGCTAATGAAGTCTCTGAAAAGTCAAAAGCTACTTCAAGTC  579
QY      408  CTACCCCTTTGACTTTCCAGGGTGCAGGATCATTTACTGCCCAGAGGAGGTGCTCTATGG  467
Db      580  CCAGCCCTTTGACTTTAGGGGTGCTCAAAATCATTTCTGGCNAAGAAAGGGGTATATGG  639
QY      468  CTGGATTAATCAATCTATCTGTGGGCAAAATTTAGTCAAGAAACAAAGGTGGTTCAAGCA  527
Db      640  ATGGATTACAGCAACTATTTAAATGGGAAATTTCTCTGGAGAAAGAACCTGTGCGCATGTG  699
QY      528  AGTCCCATATGAACCAATATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTC  587
Db      700  GGTC-----ACCCGATGGAGTGGAAACCAACCGGTGCTCTGGACTTTAGGTGGTCTC  753
QY      588  TACACAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCAGATAATGCTCTGCA  647
Db      754  CACCAATATCTCTCTGTGGCAGGAGAGAGATGAGTCTGAACACACAGGACATCATGCA  813
QY      648  ATTTGCGCTCTATGGCAAGGACTACAATGTCTTACACATAGCTTTCTGTGCTATGGGAA  707
Db      814  GGTGTCCCTGTATGGCTACGTATACACGCTCTACACACACAGCTTCCAGTGTCTATGGCG  873
QY      708  GGATCAGGCACTCTGGGAGAAACCTGGCCAGGACATTCAGGTTGCAAGTAATGAA---T  764
Db      874  GAATGAGGCTGAGAAGAAAGTTTCTGGCAATGCTCTCTGCAGAAATCTCTCACCACAAAC  933
QY      765  TCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTGAAC  824
Db      934  TCTCACCNAATCCCTGTGTACCTCGGGATTTATAGCATCAGCTTCCACATGGGCCATGATT  993
QY      825  CAAGACCCCTTGCAAC-----CAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTGA  878
Db      994  TGATAGCTGTGCACTGTGGACGAGGCCAGAAAGTTATAACCCCAATGATGTATCATCAC  1053
QY      879  AATCCAGGGTATTGGAACACTATCAACATGCCATCAAGCATCTCTGGAGCTCTTCAACAC  938
Db      1054  TTTTGAAGGAACTGGGGACCCATCTCTGTGTAAAGGAGAGGTGGCTTCCATATTTGACTT  1113
QY      939  CAGTTACTGCTTACTCCAG---TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCA  995
Db      1114  CAAAGCTTGCCATGATCAAGAAACCTGTTCTTTTGTATGGGTTTATCAGCCAAAGATTAA  1173
QY      996  GGGGGAATTTGGGCAATTTTCAAGCTTTTACTTTTGTGATGAAGTTTAAACTTCAACATC  1055
Db      1174  AGGGCCATTTGTGGCTTTTGCAGGATTTCTACTACACAGCCAGTGTCTTAAATCT---TTC  1230
QY      1056  AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTGCTCAGCCTTG  1115
Db      1231  AGGTAGCTTTTCCCTGGACACTTTCAACTCCAGCACCTTGGAAATTTCTGCTCAGAGAA  1290
QY      1116  GGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTT  1175
Db      1291  GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT  1350
QY      1176  TTCTGGTACCTACATTTCTCTCCCTCTCTCTGCAAGGCTATCATTTTCAAGCTGATTCTCTG  1235
Db      1351  CTCAGCCAATCTACATCTACCACTTTGTTGTGAACGTTTACAAATTCACAGAGGAGACTTG  1410
QY      1236  GGAGCACATCCATTTTCATTTGGCAAGATCCAGGCGAGGACGCGGCTGGACTTTGGGGTA  1295
Db      1411  GCCCAAAATACACTTTGAAAAAGAGTGGGGAATAGCAGCATAGCTGTCTCTTGGCTA  1470
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QY 1296 CATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTG 1338  
Db 1471 CATGCTCAGCCTGACCAACAGATCCAGCTGAAGCCCTCTG 1513

RESULT 14

US-09-905-743B-3  
; Sequence 3, Application US/09905743B  
; Patent No. 6828423  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; TITLE OF INVENTION: ACIDS  
; FILE REFERENCE: 28110/36120C  
; CURRENT APPLICATION NUMBER: US/09/905,743B  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-09-905-743B-3

Query Match 21.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 3.6e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;  
QY 48 CCAGAACAGCATTCGCAAAACGTTAAGTATGGATTGTCTGGATGCGGGTCTTC 107  
Db 220 CAAGCAGAGGTCTCCCTCCAGGACTGAAGTATGGTATGTCTGGATGCGGGTCTTC 279  
QY 108 TCACACAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAGGAGAAATGACACAGCGGTGGT 167  
Db 280 AAGAACACAGCTACGTGTATCAATGGCCAGCAGAAAAGGAGAAATATACCGAGTGGT 339  
QY 168 GCATCAAGTGAAGATGACGGGTAAAGTCTCGAATCTCAAAATTTGTTTCAGAAAGT 227  
Db 340 CAGTCAAAACCTTCAAAATGATGTGAAGGCTCTGGAATCTCCAGCTATGGAATAAACCC 399  
QY 228 AAATGAATAGGATTTACCTGACTGATTGTCATGGAAGAGCTAGGGAAGTGAATCCAAG 287  
Db 400 CCAAGATGTCAGAGACCTTTGAGGAGTGTATGCAAAAGTCAAGGGGAGGTTCCATC 459  
QY 288 GTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGCAGGCATCGGTTGCTCAG 347  
Db 460 CCACCTCCAGGATCCACCCCAATTCACCTGGGAGCCAGCGCTGGGATGCGCTTGCTGAG 519  
QY 348 GATGGAAGTGAAGATGTCAGAGGTTCTGGATGTGGTGGAGAGAGCCCTCAGCAA 407  
Db 520 GTTGCAAAATGAACAGCAGCTAATGAAGTCTTGAAGCATCCAAGCTACTTCAAGTC 579  
QY 408 CTACCCCTTTGACTTCCAGGTCGACAGGATCAATTAATCTGGCCAGAGAGGTCCTATGG 467  
Db 580 CCAGCCCTTTGACTTTAGGGGTGCTCAAAATCAATTTCTGGCAAGAGAGGGGTATATGG 639  
QY 468 CTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAAGGTGGTTCAGCAT 527  
Db 640 ATGGATTACAGCCCACTATTAAATGGAAATTTCTGGAGAAGAACCTGTGGCAGCATGTG 699  
QY 528 AGTCCCATATGAACCAATTAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGGAGCTC 587  
Db 700 GGTGC-----ACCCGATGGAGTGGAAACACAGGGTGCCTGGACTTAGGTGGTCTC 753  
QY 588 TACACAGTCACTTTTGTATCCCAAAACAGACATCTCGAGTCCCGCAGATAATGCTCTGCA 647

Db 754 CACCCAAATATCTCTCGTGGCAGGAGAGATGATCTGAACACACAGCGCATCATGCA 813  
QY 648 ATTTCCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGTATGGGAA 707  
Db 814 GGTGTCCCTGTATGGCTAGTATACACGCTCTACACACACAGCTTCCAGTGTCTATGGCG 873  
QY 708 GGATCAGGCACCTCTGCGAGAACTGCGCAAGGACATTCAGGTTGCAAGTAATGAAA--T 764  
Db 874 GAATGAGGCTGAGAAGAGTTTCTGGCAATGCTCTCGCAAAATTTCTCTACCAAAACCA 933  
QY 765 TCTCAGGGACCCATGCTTTTCATCTCGATATAGAAGGTAGTGAACGTAAAGTGAACCTTTA 824  
Db 934 TCTCACCATCTCTGTACCTCGGATTTATAGCATCAGCTTCCACATGGGCCATGTAAT 993  
QY 825 CAAGACCCCTGCAC-----CAAGAGATTTGAGATGACTCTTCCATTCACAGCAGTTGA 878  
Db 994 TGATAGCCTGTGCACTGTGGACAGAGGCCAGAAAGTTATAAACCCCAATGATGTCAATC 1053  
QY 879 AATCCAGGCTATTGGAAACTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACAC 938  
Db 1054 TTTTGAAGNACTGGGACCCATCTCTGTGTAAAGAGAGGTGGCTTCCATTAATTTGACTT 1113  
QY 939 CAGTTACTGCCCTTACTCCAG---TGTGCTTCAATGGGATTTTCTTCCACCACCTCCA 995  
Db 1114 CAAAGCTTGCCATGATCAAGAAACCTGTTCTTTTGTATGGGTTTATCAGCCAAAGATTAA 1173  
QY 996 GGGGATTTTGGGCAATTTTTCAGCTTTTTCATCTTGTGATGAAGTTTTHAACTTGACATC 1055  
Db 1174 AGGGCCATTTTGTGGCTTTTTCAGGATTTCTACTACACAGCCAGTGTCTTTAAATCT--TTC 1230  
QY 1056 AGAAGAGTCTCTCAGGAAAGGTGCTGAGATGATGAAAAGTTCTGTGCTCAGCCTTG 1115  
Db 1231 AGGTAGCTTTTCCCTGGACACCTTCACTCCAGCACCTGGAATTTCTGCTCAGAGATTG 1290  
QY 1116 CGAGGAGATATAAACAATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTT 1175  
Db 1291 GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGATGAGGTATATGCCGCTCTTACTGCTT 1350  
QY 1176 TTCTGGTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTCCTG 1235  
Db 1351 CTCAGCCAACTACATCTACCACTTGTGTTGTAACGGTTACAAATTCACAGAGAGACTTG 1410  
QY 1236 GGAGCACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGCTGGACTTTGGGCTA 1295  
Db 1411 GCCCAATACACTTTGAAAAGAGTGGGGAATAGCAGCATAGCTGCTGCTCTTGGCTA 1470  
QY 1296 CATGCTGAACCTGACCAACATGATCCAGCTCAGCAACCATTTG 1338  
Db 1471 CATGCTCAGCCTGACCAACAGATCCAGCTGAAAAGCCCTCTG 1513

RESULT 15

US-09-949-016-13848  
; Sequence 13848, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13848  
; LENGTH: 46885

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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(46885)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13848

Query Match      19.8%; Score 270.2; DB 4; Length 46885;
Best Local Similarity 98.9%; Pred. No. 2.8e-78;
Matches 272; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      741 CATTGAGGTGCAAGTAATGAATTCCTCAGGGACCCATGCTTTCATCCTGGATATAAGAA 800
Db      26315 CATTGAGGTGCAAGTAATGAATTCCTCAGGGACCCATGCTTTCATCCTGGATATAAGAA 26374

Qy      801 GGTAGTGAACGTAAAGTGACCTTTTACAAGACCCCTGCACCAAGAGATTTGAGATGACTCT 860
Db      26375 GGTAGTGAACGTAAAGTGACCTTTTACAAGACCCCTGCACCAAGAGATTTGAGATGACTCT 26434

Qy      861 TCCATTCCAGCAGTTTGAATCCAGGGTATTTGGAAACTATCAACAATGCCATCAAAGCAT 920
Db      26435 TCCATTCCAGCAGTTTGAATCCAGGGTATTTGGAAACTATCAACAATGCCATCAAAGCAT 26494

Qy      921 CTGGAGCTCTTCAACACACAGTTTACTGCCCTTACTCCCAAGTGTGCCTTCAATGGGATTTT 980
Db      26495 CTGGAGCTCTTCAACACACAGTTTACTGCCCTTACTCCCAAGTGTGCCTTCAATGGGATTTT 26554

Qy      981 CTTGCCACCACCTCCAGGGGATTTTGGGGCATTTT 1015
Db      26555 CTTGCCACCACCTCCAGGGGATTTTGGGGTAAGTT 26589
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Search completed: September 21, 2005, 23:30:30  
Job time : 251.55 secs

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**THIS PAGE BLANK (USPTO)**





; NAME/KEY: CDS									
; LOCATION: (1)..(1362)									
US-09-835-147-5									
Query Match 100.0%; Score 1365; DB 9; Length 1365;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GCACCTACTTCAAGTGTCTACAAAGAAAAACACAGCTAACTAGTTTCAACCCAGCAACAAAGCA	60						
Db	1	GCACCTACTTCAAGTGTCTACAAAGAAAAACACAGCTAACTAGTTTCAACCCAGCAACAAAGCA	60						
Qy	61	TTGCCAGAAACCTTAAGTATGGATTGTGCTGATGCGGGTTCTTCTCACACAAGTTTA	120						
Db	61	TTGCCAGAAACCTTAAAGTATGGATTGTGCTGATGCGGGTTCTTCTCACACAAGTTTA	120						
Qy	121	TACATCTATAAGTGGCCAGCAGAAAAAGGAGAATGACACAGCGGTGGTGCATCAAGTAGAA	180						
Db	121	TACATCTATAAGTGGCCAGCAGAAAAAGGAGAATGACACAGCGGTGGTGCATCAAGTAGAA	180						
Qy	181	GAATGACAGGGTTAAGGTCCTGGAATCTCAAAATTTTGTTCAGAAAAGTAATGAATAGGC	240						
Db	181	GAATGACAGGGTTAAGGTCCTGGAATCTCAAAATTTTGTTCAGAAAAGTAATGAATAGGC	240						
Qy	241	ATTTACTGACTGATTGCAATGGAAAGAGCTAGGGAAGTGAATCCAAAGTCCCAAGACCAA	300						
Db	241	ATTTACTGACTGATTGCAATGGAAAGAGCTAGGGAAGTGAATCCAAAGTCCCAAGACCAA	300						
Qy	301	GAGACACCCCTTTACCTGGGAGCCAGCGAGCATCGGTTGCTCAGGATGGAAAGTGAA	360						
Db	301	GAGACACCCCTTTACCTGGGAGCCAGCGAGCATCGGTTGCTCAGGATGGAAAGTGAA	360						
Qy	361	GAGTTGGCAGACAGGGTTCTGGAATGTGGTGGAGAGGCCCTCAGAACTACCCCTTTGAC	420						
Db	361	GAGTTGGCAGACAGGGTTCTGGAATGTGGTGGAGAGGCCCTCAGAACTACCCCTTTGAC	420						
Qy	421	TTCCAGGTGCCAGGATCATTACTGCCAAGAGAGAGGTCCTATCGCTGGATTACTATC	480						
Db	421	TTCCAGGTGCCAGGATCATTACTGCCAAGAGAGAGGTCCTATCGCTGGATTACTATC	480						
Qy	481	AACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGTTTCAGCATAGTCCCATATGAA	540						
Db	481	AACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGTTTCAGCATAGTCCCATATGAA	540						
Qy	541	ACCAATAATCAGAAACCTTTGAGCTTTTGGACCTTTGGGGAGGCCCTTACAAAGTCACT	600						
Db	541	ACCAATAATCAGAAACCTTTGAGCTTTTGGACCTTTGGGGAGGCCCTTACAAAGTCACT	600						
Qy	601	TTTGTACCCCAAAACCAAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTGSCCTCTAT	660						
Db	601	TTTGTACCCCAAAACCAAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTGSCCTCTAT	660						
Qy	661	GGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGGAAGGATCAGGCACTC	720						
Db	661	GGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGGAAGGATCAGGCACTC	720						
Qy	721	TGGCAGAAATCGGCCAAGGACATTCAGGTTTGAAGTAATGAATTTCTCAGGGACCCATGC	780						
Db	721	TGGCAGAAATCGGCCAAGGACATTCAGGTTTGAAGTAATGAATTTCTCAGGGACCCATGC	780						
Qy	781	TTTTCATCCTGGATATAGAGAGTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	840						
Db	781	TTTTCATCCTGGATATAGAGAGTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	840						
Qy	841	AAGAGATTTTGAATGACTCTTCCATCCAGCAGTTTGAATCCAGGGTATTTGGAATCTAT	900						
Db	841	AAGAGATTTTGAATGACTCTTCCATCCAGCAGTTTGAATCCAGGGTATTTGGAATCTAT	900						
Qy	901	CAACAATGCCATCAAGACATCTCGAGCTCTTCAACACCAAGTTACTGCCCCTTACTCCCAG	960						
Db	901	CAACAATGCCATCAAGACATCTCGAGCTCTTCAACACCAAGTTACTGCCCCTTACTCCCAG	960						
Qy	961	TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCT	1020						

Db	961	TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCT	1020						
Qy	1021	TTTTACTTTGTGATGAAGTTTTTAAACTTTGAACATCAGAGAAAAGTCTCTCAGGAAAAGGTG	1080						
Db	1021	TTTTACTTTGTGATGAAGTTTTTAAACTTTGAACATCAGAGAAAAGTCTCTCAGGAAAAGGTG	1080						
Qy	1081	ACTGAGATGATCAAAAAGTTTCTGCTCAGCCTTGGGAGGAGATAAAAACATCTTACGCT	1140						
Db	1081	ACTGAGATGATCAAAAAGTTTCTGCTCAGCCTTGGGAGGAGATAAAAACATCTTACGCT	1140						
Qy	1141	GGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTTACATTTCTCCCTC	1200						
Db	1141	GGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTTACATTTCTCCCTC	1200						
Qy	1201	CTTCTGCAAGGCTATCATTTTCAAGCTGATTCCTGGAGCACATCCATTTCAATTTGCGCAAG	1260						
Db	1201	CTTCTGCAAGGCTATCATTTTCAAGCTGATTCCTGGAGCACATCCATTTCAATTTGCGCAAG	1260						
Qy	1261	ATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC	1320						
Db	1261	ATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC	1320						
Qy	1321	CCAGCTGAGCAACCACTTTGTCCACACCTCTCTCCCACTCCACCTAA	1365						
Db	1321	CCAGCTGAGCAACCACTTTGTCCACACCTCTCTCCCACTCCACCTAA	1365						

RESULT 2

US-09-835-147-7

; Sequence 7, Application US/09835147

; Patent No. US20020002277A1

; GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R.

; APPLICANT: Gayle III, Richard B.

; APPLICANT: Price, Virginia L.

; APPLICANT: Gimpel, Steven D.

; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

; FILE REFERENCE: 2879-US

; CURRENT APPLICATION NUMBER: US/09/835,147

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/104,585

; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: US 60/149,010

; PRIOR FILING DATE: 1999-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/22955

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1437

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion

; OTHER INFORMATION: construct of human CD39

; NAME/KEY: CDS

; LOCATION: (1)..(1434)

US-09-835-147-7

Query Match 100.0%; Score 1365; DB 9; Length 1437;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCTACTTCAAGTGTCTACAAAGAAAAACACAGCTAACTAGTTTCAACCCAGCAACAAAGCA 60

Db 73 GCACCTACTTCAAGTGTCTACAAAGAAAAACACAGCTAACTAGTTTCAACCCAGCAACAAAGCA 132

Qy 61 TTGCCAGAAAAAGCTTAAAGTATGGGATTTGTGCTGGATGCGGGTTCTTCTCACACAAGTTTA 120

Db 133 TTGCCAGAAAAAGCTTAAAGTATGGGATTTGTGCTGGATGCGGGTTCTTCTCACACAAGTTTA 192

QY 121 TACATCTATAAGTGGCCAGCAGAGAAAGGAGATGACACAGGCGTGGTGCATCAAGTAGAA 180  
DB 193 TACATCTATAAGTGGCCAGCAGAGAAAGGAGATGACACAGGCGTGGTGCATCAAGTAGAA 252  
QY 181 GAATGACAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGC 240  
DB 253 GAATGACAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGC 312  
QY 241 ATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGATTCGAAGTCCAGCAGACCAA 300  
DB 313 ATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGATTCGAAGTCCAGCAGACCAA 372  
QY 301 GAGACACCCGTTTACCTGGGAGCCAGCGAGGATGCGGTTGCTCAGGATGGAAGTGA 360  
DB 373 GAGACACCCGTTTACCTGGGAGCCAGCGAGGATGCGGTTGCTCAGGATGGAAGTGA 432  
QY 361 GAGTTGGCAGACAGGTTCTGATGTGGTGGAGAGGCGCTCAGCAACTACCCCTTGC 420  
DB 433 GAGTTGGCAGACAGGTTCTGATGTGGTGGAGAGGCGCTCAGCAACTACCCCTTGC 492  
QY 421 TTCCAGGTCGCCAGGATCAATTAAGTCCAGAGGAGGTCCTATGCGCTGGATTAATC 480  
DB 493 TTCCAGGTCGCCAGGATCAATTAAGTCCAGAGGAGGTCCTATGCGCTGGATTAATC 552  
QY 481 AACTATCTGCTGGGCAAAATTCAGTTCAGAAAAACAAGTGGTTCCAGCATAGTCCCATATGAA 540  
DB 553 AACTATCTGCTGGGCAAAATTCAGTTCAGAAAAACAAGTGGTTCCAGCATAGTCCCATATGAA 612  
QY 541 ACCAATATCAGAAACCTTTGGAGCTTTGGACCTTTGGGGAGGCTTACACAACTCACT 600  
DB 613 ACCAATATCAGAAACCTTTGGAGCTTTGGACCTTTGGGGAGGCTTACACAACTCACT 672  
QY 601 TTGTACCCCAAAACAGACTATCAGTCCCGAGATAATGCTCTGCAATTTCCGCTCTAT 660  
DB 673 TTGTACCCCAAAACAGACTATCAGTCCCGAGATAATGCTCTGCAATTTCCGCTCTAT 732  
QY 661 GCGAAGGACTACAATGTGTACACACATAGCTTTCTTGTCTATGGGAAGGATCAGGACTC 720  
DB 733 GCGAAGGACTACAATGTGTACACACATAGCTTTCTTGTCTATGGGAAGGATCAGGACTC 792  
QY 721 TGGCAGAACTGCGCCAGAGACATTCAGTTGCAAGTAAATGAAATTCACGGGACCCATGC 780  
DB 793 TGGCAGAACTGCGCCAGAGACATTCAGTTGCAAGTAAATGAAATTCACGGGACCCATGC 852  
QY 781 TTTCATCTGGATATAAGAGGTTAGTGAACGTAAAGTGACCTTTTCAAGACCCCTGCACC 840  
DB 853 TTTCATCTGGATATAAGAGGTTAGTGAACGTAAAGTGACCTTTTCAAGACCCCTGCACC 912  
QY 841 AAGAGATTGAGATGACTCTTCCATTCACGAGTTTGAATCCAGGGTATTGGAAACTAT 900  
DB 913 AAGAGATTGAGATGACTCTTCCATTCACGAGTTTGAATCCAGGGTATTGGAAACTAT 972  
QY 901 CAACAATGCCATCAAGGATCTGAGCTCTTCAACACAGTTACTGCGCTTACTCCAG 960  
DB 973 CAACAATGCCATCAAGGATCTGAGCTCTTCAACACAGTTACTGCGCTTACTCCAG 1032  
QY 961 TGTGCTTTCAATGGATTTTCTTGCACACTCCAGGGGGATTTTGGGGCATTTTCAGCT 1020  
DB 1033 TGTGCTTTCAATGGATTTTCTTGCACACTCCAGGGGGATTTTGGGGCATTTTCAGCT 1092  
QY 1021 TTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1080  
DB 1093 TTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1152  
QY 1081 ACTGAGATGAAAAAGTTCTGTGCTCAGCCCTGGGAGGAGATAAAAACATCTTACGCT 1140  
DB 1153 ACTGAGATGAAAAAGTTCTGTGCTCAGCCCTGGGAGGAGATAAAAACATCTTACGCT 1212  
QY 1141 GGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTGTGTACCTACTCTCCCTC 1200  
DB 1213 GGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTGTGTACCTACTCTCCCTC 1272

RESULT 3

US-09-835-147-25  
; Sequence 25, Application US/09835147  
; Patent No. US2002002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 1464  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1461)  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
; OTHER INFORMATION: construct of human CD39  
US-09-835-147-25

Query Match 97.3%; Score 1328; DB 9; Length 1464;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1334; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 11 CAAGTTCTACAAAGAAAACACAGCTAACTAGTTCACCCAGAACAAAGCATTTGCCAGAAA 70  
DB 110 CTAGTTCAGGAGACTACAAAGATGACGATGACAAACCAGAACAAAGCATTTGCCAGAAA 169  
QY 71 ACGTTAAGTATGGGATTTGCTGGATGCGGGTTCTTCTCACACAAGTTTATACATCTATA 130  
DB 170 ACGTTAAGTATGGGATTTGCTGGATGCGGGTTCTTCTCACACAAGTTTATACATCTATA 229  
QY 131 AGTGCCAGCAGAAAAAGGAGAAATGACACAGCGGTGGTGCATCAAGTAGAAGATGCAGGG 190  
DB 230 AGTGCCAGCAGAAAAAGGAGAAATGACACAGCGGTGGTGCATCAAGTAGAAGATGCAGGG 289  
QY 191 TTAAGGTCTCGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAAATAGGCATTTTACCTGA 250  
DB 290 TTAAGGTCTCGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAAATAGGCATTTTACCTGA 349  
QY 251 CTGATTGATGGAAGAGCTAGGGAAGTGAATTCAGAGTCCAGCACCAGAGACACCCG 310  
DB 350 CTGATTGATGGAAGAGCTAGGGAAGTGAATTCAGAGTCCAGCACCAGAGACACCCG 409  
QY 311 TTTACCTGGGAGCCAGCGCAGGCATGCGGTTGCTCAGAGTGGAAAGTGAAGTTGGCAG 370

410 TTTTACCTGGAGCCACGGCAGGCATGCGGTGCTCAGATGGAAAGTGGAAGAGTTGGCAG 469  
QY ACAGGGTTCTGGATGTGGTGAGAGAGCCTCAGCAACTACCCCTTTGACTTCCAGGGTG 430  
Db ACAGGGTTCTGGATGTGGTGAGAGAGCCTCAGCAACTACCCCTTTGACTTCCAGGGTG 529  
QY CCAGGATCATTAATCTGGCCAAAGAGGAGGCTGCTATGGCTGGATTAATCACTCAACTATCTGC 490  
Db CCAGGATCATTAATCTGGCCAAAGAGAGGAGGCTGCTATGGCTGGATTAATCACTCAACTATCTGC 589  
QY TGGGCAAAATTCAGTCAGAAACAAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAATC 550  
Db TGGGCAAAATTCAGTCAGAAACAAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAATC 649  
QY AGAAACCTTTGGAGCTTTGGACCTTTGGGGGAGCCTCTACACAAGTCACTTTGTACCCC 610  
Db AGAAACCTTTGGAGCTTTGGACCTTTGGGGGAGCCTCTACACAAGTCACTTTGTACCCC 709  
QY AAAACACAGACTATCGAGTCCCCAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACT 670  
Db AAAACACAGACTATCGAGTCCCCAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACT 769  
QY ACAATGTCTACACATAGCTTTCTGTGCTATGGAAGGATCAGGCACCTCGGCAGAAAC 829  
Db ACAATGTCTACACATAGCTTTCTGTGCTATGGAAGGATCAGGCACCTCGGCAGAAAC 829  
QY TGGCCCAAGGACATTCAGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTTTCATCCTG 790  
Db TGGCCCAAGGACATTCAGTTGCAAGTAATGAAATTTCTCAGGAGCCCATGCTTTTCATCCTG 889  
QY GATATGAAGAGTAGTGAACGTAAAGTGACCTTTTACAAGACCCCTGCAACAGAGATTG 850  
Db GATATGAAGAGTAGTGAACGTAAAGTGACCTTTTACAAGACCCCTGCAACAGAGATTG 949  
QY AGATGACTCTTCCATTCAGCAGCTTTGAAATCCAGGGTATGGAATCTATCAACAATGCC 910  
Db AGATGACTCTTCCATTCAGCAGCTTTGAAATCCAGGGTATGGAATCTATCAACAATGCC 1009  
QY ATCAAGACATCTGGAGCTTTCAACACAGATTACTGCGCTTACTCCAGTGCGCTTCA 970  
Db ATCAAGACATCTGGAGCTTTCAACACAGATTACTGCGCTTACTCCAGTGCGCTTCA 1069  
QY ATGGGATTTTCTGCGCACCACTCCAGGGGATTTTGGGGCATTTTCAGCTTTTACTTTG 1030  
Db ATGGGATTTTCTGCGCACCACTCCAGGGGATTTTGGGGCATTTTCAGCTTTTACTTTG 1129  
QY TGATGAAGTTTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGA 1090  
Db TGATGAAGTTTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGA 1189  
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Db TGAAGAGTTCTGTCTCAGCCTTGGAGAGATTAACAATCTTACGCTGGAGTAAAGG 1249  
QY AGAAGTACCTGAGTGAATCTGCTTTCTGGTACCTACATTTCTCCCTCTTTCTGCAAG 1210  
Db AGAAGTACCTGAGTGAATCTGCTTTCTGGTACCTACATTTCTCCCTCTTTCTGCAAG 1309  
QY GCTATCAATTTACAGCTGATTTCTGGAGCACAATCAATTTTCAATTTGCAAGGCA 1270  
Db GCTATCAATTTACAGCTGATTTCTGGAGCACAATCAATTTTCAATTTGCAAGGCA 1369  
QY GCACGCCGCTGAGCTTTGGGCTACATGCTGAACCTGACCAATGATCCGAGCTGAGC 1330  
Db GCACGCCGCTGAGCTTTGGGCTACATGCTGAACCTGACCAATGATCCGAGCTGAGC 1429  
QY AACCATTTGTCACACCTCTCTCTCCACCTCA 1365  
Db AACCATTTGTCACACCTCTCTCTCCACCTCA 1464

; Sequence 1, Application US/09835147  
; Patent No. US20020002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(1596)  
; US-09-835-147-1

Query Match 96.6%; Score 1319.2; DB 9; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATTCGG 100  
Db 173 GGTGTGACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATTCGG 232  
QY 101 GTTCTTCTCACACAGTTTATACATCTAAGTGGCCAGACAGAAAAAGGAGAAATGACACAG 160  
Db 233 GTTCTTCTCACACAGTTTATACATCTAAGTGGCCAGACAGAAAAAGGAGAAATGACACAG 292  
QY 161 GGTGTGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTT 220  
Db 293 GGTGTGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTT 352  
QY 221 AGAAAGTAAATGAATATAGGCATTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGA 280  
Db 353 AGAAAGTAAATGAATATAGGCATTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGA 412  
QY 281 TTCCAGGTTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGATCCGGT 340  
Db 413 TTCCAGGTTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGATCCGGT 472  
QY 341 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGTGTGGAGAGGAGCC 400  
Db 473 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGTGTGGAGAGGAGCC 532  
QY 401 TCAGCAACTACCCCTTTTGAATTCCTCAGGGTGCAGAGATCAATTAATCTGCCCAAGAGGAGGTTG 460  
Db 533 TCAGCAACTACCCCTTTTGAATTCCTCAGGGTGCAGAGATCAATTAATCTGCCCAAGAGGAGGTTG 592  
QY 461 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAAGAAAAACAAGTGGT 520  
Db 593 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAAGAAAAACAAGTGGT 652  
QY 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
Db 653 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 712  
QY 581 GAGCCTCTACACAGTCACTTTTGTATCCCAAAAACAGACTATTCAGTCCCAAGATAATG 640  
Db 713 GAGCCTCTACACAGTCACTTTTGTATCCCAAAAACAGACTATTCAGTCCCAAGATAATG 772

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QY 641 CTCTGCAATTTGGCCTCTATGGCAAGGACTACAAATCTCTACACACATAGCTTCTTGTC 700
Db 773 CTCTGCAATTTGGCCTCTATGGCAAGGACTACAAATCTCTACACACATAGCTTCTTGTC 832
QY 701 ATGGGAAGGATCAGGCACCTCTGCACAAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 760
Db 833 ATGGGAAGGATCAGGCACCTCTGCAGAAATGCGCAAGGACATTCAGGTTGCAAGTAATG 892
QY 761 AAATCTCAGGACCCATCTTTTCATCTGGATATAAGGAAGGTAGTGAACGTAAGTGACC 820
Db 893 AAATCTCAGGACCCATCTTTTCATCTGGATATAAGGAAGGTAGTGAACGTAAGTGACC 952
QY 821 TTTACAAGACCCCTGCAACAAGATTTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 880
Db 953 TTTACAAGACCCCTGCAACAAGATTTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1012
QY 881 TCCAGGATTTGGAACTATCAACATGCATCAAGCATCTGGAGCTTTCACACCA 940
Db 1013 TCCAGGATTTGGAACTATCAACATGCATCAAGCATCTGGAGCTTTCACACCA 1072
QY 941 GTTACTGCCCTTACTCCCACTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1000
Db 1073 GTTACTGCCCTTACTCCCACTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1132
QY 1001 ATTTTGGGCAATTTTCAGCTTTTACTTTTGATGAAGTTTAACTTGACATCAGAGA 1060
Db 1133 ATTTTGGGCAATTTTCAGCTTTTACTTTTGATGAAGTTTAACTTGACATCAGAGA 1192
QY 1061 AGTCTCTCAGAAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGAGG 1120
Db 1193 AGTCTCTCAGAAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGAGG 1252
QY 1121 AGATAAAACATCTTACGCTGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTTCTG 1180
Db 1253 AGATAAAACATCTTACGCTGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTTCTG 1312
QY 1181 GTACTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTGGAGC 1240
Db 1313 GTACTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTGGAGC 1372
QY 1241 ACATCATTTTCAATGGCAAGATCCAGGGCAGGACCGCGCTGGACTTTGGCTACATGC 1300
Db 1373 ACATCATTTTCAATGGCAAGATCCAGGGCAGGACCGCGCTGGACTTTGGCTACATGC 1432
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1360
Db 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1492
QY 1361 CCTA 1364
Db 1493 CCTA 1496
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RESULT 5

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US-10-646-308-29
; Sequence 29, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 1599
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(1596)
US-10-646-308-29
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Query Match 96.6%; Score 1319.2; DB 19; Length 1599;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTGCTTGGATGCCG 100
Db 173 GGTTGACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTGCTTGGATGCCG 232
QY 101 GTTCTTCTCACAAAGTTTATACATCTATAGTGGCCAGCAGAAAGGAGAAATGACACAG 160
Db 233 GTTCTTCTCACAAAGTTTATACATCTATAGTGGCCAGCAGAAAGGAGAAATGACACAG 292
QY 161 GCGTGGTGCATCAAGTAGAAGAAATGACAGGTTTAAAGGTTCTTGGAAATCTCAAAAATTTGTTT 220
Db 293 GCGTGGTGCATCAAGTAGAAGAAATGACAGGTTTAAAGGTTCTTGGAAATCTCAAAAATTTGTTT 352
QY 221 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTCGATGCGAAAGAGCTAGGGAAGTGA 280
Db 353 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTCGATGCGAAAGAGCTAGGGAAGTGA 412
QY 281 TTCCAAGGTGCCAGCACCAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCAATGCGGT 340
Db 413 TTCCAAGGTGCCAGCACCAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCAATGCGGT 472
QY 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTTCTGGATGTGGTGGAGAGAGCC 400
Db 473 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTTCTGGATGTGGTGGAGAGAGCC 532
QY 401 TCAGCAACTACCCCTTTGACCTTCAGGCTGCCAGGATCATTTACTGCGCCAGAGGAAGTG 460
Db 533 TCAGCAACTACCCCTTTGACCTTCAGGCTGCCAGGATCATTTACTGCGCCAGAGGAAGTG 592
QY 461 CCTATGGCTGGATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 520
Db 593 CCTATGGCTGGATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 652
QY 521 TCAGCATAGTCCCATATGAAACCAATATTCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580
Db 653 TCAGCATAGTCCCATATGAAACCAATATTCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 712
QY 591 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAGATAATG 640
Db 713 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAGATAATG 772
QY 641 CTCTGCAATTTGGCCTCTATGGCAAGGACTACAAATCTCTACACACATAGCTTCTTGTC 700
Db 773 CTCTGCAATTTGGCCTCTATGGCAAGGACTACAAATCTCTACACACATAGCTTCTTGTC 832
QY 701 ATGGGAAGGATCAGGCACCTCTGGCAGAAAATGCGCAAGGACATTCAGGTTGCAAGTAATG 760
Db 833 ATGGGAAGGATCAGGCACCTCTGGCAGAAAATGCGCAAGGACATTCAGGTTGCAAGTAATG 892
QY 761 AAATTTCTCAGGACCCATCTTTTCATCTCGATATAAGGAAGGTAGTGAACGTAAGTGACC 820
Db 893 AAATTTCTCAGGACCCATCTTTTCATCTCGATATAAGGAAGGTAGTGAACGTAAGTGACC 952
QY 821 TTTACAAGACCCCTGCAACAAGATTTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 880
Db 953 TTTACAAGACCCCTGCAACAAGATTTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1012
QY 881 TCCAGGATTTGGAACTATCAACATGCATCAAGCATCTGGAGCTTTCACACCA 940
Db 1013 TCCAGGATTTGGAACTATCAACATGCATCAAGCATCTGGAGCTTTCACACCA 1072
QY 941 GTTACTGCCCTTACTCCCACTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1000
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Db 1073 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGG 1132  
Qy 1001 ATTTGGGGCATTTTCAAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1060  
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Qy 1061 AAGTCTCTCAGGAAAGGTGACATGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGAGG 1120  
Db 1193 AAGTCTCTCAGGAAAGGTGACATGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGAGG 1252  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1180  
Db 1253 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1312  
Qy 1181 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGGAGC 1240  
Db 1313 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGGAGC 1372  
Qy 1241 ACATCCATTTTATTTGGCAAGATCCAGGCGAGCGACGCGCTGGACTTTTGGGCTACATGC 1300  
Db 1373 ACATCCATTTTATTTGGCAAGATCCAGGCGAGCGACGCGCTGGACTTTTGGGCTACATGC 1432  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCACACCTCTCTCCCACTCCA 1360  
Db 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCACACCTCTCTCCCACTCCA 1492  
Qy 1361 CCTA 1364  
Db 1493 CCTA 1496

## RESULT 6

US-10-643-1475  
; Sequence 1475, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1475:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g765255  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1475 :  
US-10-643-1475  
Query Match 96.6%; Score 1319.2; DB 18; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAAGTATGGGATTTGTCTGGATCGG 100  
Db 174 GGTGACCCAGAACAAAGCATTTGCCAGAAAACGTTAAAGTATGGGATTTGTCTGGATCGG 233  
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 160  
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 293  
Qy 161 GCGTGTGCATCAAGTATGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
Db 294 GCGTGTGCATCAAGTATGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
Qy 221 AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTGCAATGGAAGAGCTAGGGAAGTGA 280  
Db 354 AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTGCAATGGAAGAGCTAGGGAAGTGA 413  
Qy 281 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACTTGGAGGCCAGCGGAGGATCCGGT 340  
Db 414 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACTTGGAGGCCAGCGGAGGATCCGGT 473  
Qy 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGGAGAGAGGCC 400  
Db 474 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGGAGAGAGGCC 533  
Qy 401 TCAGCAACTACCCCTTTTGACTTCCAGGGTGCAGAGATCAATTACTGCCCAAGAGGAGGTG 460  
Db 534 TCAGCAACTACCCCTTTTGACTTCCAGGGTGCAGAGATCAATTACTGCCCAAGAGGAGGTG 593  
Qy 461 CTATGGCTGGATTTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 520  
Db 594 CCTATGGCTGGATTTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 653  
Qy 521 TCAGCATAGTCCCATATGAACCAATATCAAGAACCTTTGGAGCTTTGGACCTTTGGGG 580  
Db 654 TCAGCATAGTCCCATATGAACCAATATCAAGAACCTTTGGAGCTTTGGACCTTTGGGG 713  
Qy 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAGATAATG 640  
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Qy 641 CTCTGCAATTCGCTCTATGGCAAGGACTACATGTCTACACATAGCTTCTTGTGCT 700  
Db 774 CTCTGCAATTCGCTCTATGGCAAGGACTACATGTCTACACATAGCTTCTTGTGCT 833  
Qy 701 ATGGGAAGGATCAGGCACCTCTCGCAAACTCGCCAAAGGACATTCAGGTTGCAAGTAATG 760  
Db 834 ATGGGAAGGATCAGGCACCTCTCGCAAACTCGCCAAAGGACATTCAGGTTGCAAGTAATG 893  
Qy 761 AAATTCCTCAGGGACCCATGCTTTTCTCTGGATATAAAGAGGTAGTGAACGTAAAGTACC 820  
Db 894 AAATTCCTCAGGGACCCATGCTTTTCTCTGGATATAAAGAGGTAGTGAACGTAAAGTACC 953  
Qy 821 TTTCAGAACCCCTTGCACCAAGAGATTTGAGATGACTCTTCATCTCCAGCAGCTTTGAAA 880  
Db 954 TTTCAGAACCCCTTGCACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGCTTTGAAA 1013  
Qy 881 TCCAGGGTATTGGAAACTATCAACATGCATCAAGAGCTCTGGAGCTCTTCAACACCA 940  
Db 1014 TCCAGGGTATTGGAAACTATCAACATGCATCAAGAGCTCTGGAGCTCTTCAACACCA 1073  
Qy 941 GTTACTGCCCTTACTCCCAAGTGTGCCTTCAATGGGATTTTCTTGGCACCACCTCCAGGGG 1000

Db 1074 GTTACTGCCCTTACTCCAGTGTGCCCTCAATGGGATTTCTTGGCCACCACTCCAGGGGG 1133  
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Db 1134 ATTTGGGCAATTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1193  
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Db 1194 AGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCTGTGCTAGCCTTGGGAGG 1253  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTCTG 1180  
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Db 1314 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTACAGCTGATTCCTGGAGC 1373  
Qy 1241 ACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1300  
Db 1374 ACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGCCACACTCTCTCCCACTCCA 1360  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGCCACACTCTCTCCCACTCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497

RESULT 7  
US-10-934-998-290  
; Sequence 290, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 290  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Genbank/S73813  
; DATABASE ENTRY DATE: 1995-04-12  
US-10-934-998-290

Query Match 96.6%; Score 1319.2; DB 22; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCAGAACAAAGCATTTGCCAGAAAAGCTTAAGTATGGGATTTGTGCTGATGCGG 100  
Db 174 GGTTCACCCAGAACAAAGCATTTGCCAGAAAAGCTTAAGTATGGGATTTGTGCTGATGCGG 233  
Qy 101 GTTCTTCTCACAGATTTTATACATCTATAGTGGCCAGCAGAAAGAGATGACACAG 160  
Db 234 GTTCTTCTCACAGATTTTATACATCTATAGTGGCCAGCAGAAAGAGATGACACAG 293

Qy 161 GCGTGGTGCATCAAGATAGAGAAATCAGGGTTAAAGGTCCTTGGAAATCTCAAAATTTGTTTC 220  
Db 294 GCGTGGTGCATCAAGATAGAGAAATCAGGGTTAAAGGTCCTTGGAAATCTCAAAATTTGTTTC 353  
Qy 221 AGAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAGTCA 280  
Db 354 AGAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAGTGA 413  
Qy 281 TTCCAAGGTCCAGCACCAGAGACACCCGTTTACCTGGAGGCCACGGCAGGCATCGCGT 340  
Db 414 TTCCAAGGTCCAGCACCAGAGACACCCGTTTACCTGGAGGCCACGGCAGGCATCGCGT 473  
Qy 341 TGCTCAGGATGGAAGTGAAGTGGCAGACAGGGTTCCTGATGTGTGGAGAGAGCC 400  
Db 474 TGCTCAGGATGGAAGTGAAGTGGCAGACAGGGTTCCTGATGTGTGGAGAGAGCC 533  
Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGGCCAAAGGAGGTTG 460  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGGCCAAAGGAGGTTG 593  
Qy 461 CCTATGGCTGGATTAATACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 520  
Db 594 CCTATGGCTGGATTAATACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 653  
Qy 521 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGAGCTTTGGGG 580  
Db 654 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGAGCTTTGGGG 713  
Qy 581 GAGCCTCTACACAGTCACTTTTGTACCCCAAAACCAGACTATCAGTCCCAAGTAATG 640  
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Qy 641 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 700  
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Qy 701 ATGGAAAGATCAGGCACCTCTGGCAGAAACTGGCCAAAGCAATTCAGTGTGCAAGTAATG 760  
Db 834 ATGGAAAGATCAGGCACCTCTGGCAGAAACTGGCCAAAGCAATTCAGTGTGCAAGTAATG 893  
Qy 761 AAATTTCTCAGGAGCCCATGCTTTTCTCTGATATAGAAGTGTAGCTTAAGTGAAC 820  
Db 894 AAATTTCTCAGGAGCCCATGCTTTTCTCTGATATAGAAGTGTAGCTTAAGTGAAC 953  
Qy 821 TTTTCAAGACCCCTTGCAACCAAGAGATTGAGATGACTCTTCCATTCCAGCAGATTTGAAA 880  
Db 954 TTTTCAAGACCCCTTGCAACCAAGAGATTGAGATGACTCTTCCATTCCAGCAGATTTGAAA 1013  
Qy 881 TCCAGGGTATTTGGAAAACCTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACACCA 940  
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Qy 1001 ATTTTGGGGCAATTTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1060  
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Qy 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTTGGGAGG 1120  
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Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG 1313  
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Db 1374 ACATCAATTCATTTGGCAAGATCCAGGCGACGACGCGGCTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCACACCTCTCTCCCACTCCA 1360  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCACACCTCTCTCCCACTCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497

RESULT 8  
US-10-934-998-46  
; Sequence 46, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934, 998  
; PRIOR FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: Patencin version 3.2  
; SEQ ID NO 46  
; LENGTH: 2081  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: GS-N45  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GENBANK/AJ131313  
; DATABASE ENTRY DATE: 2000-01-19  
; RELEVANT RESIDUES: (1)..(2081)  
US-10-934-998-46

Query Match 96.6%; Score 1319.2; DB 22; Length 2081;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCCAGAACAAAGCAATGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGG 100  
Db 311 GGTGACCCAGAACAAAGCAATGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGG 370  
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 160  
Db 371 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 430  
Qy 161 GCCTGGTGCATCAAGTAGAAGATGACAGGGTTAAAGGCTCTGGAATCTCAAAAATTTGTTT 220  
Db 431 GCCTGGTGCATCAAGTAGAAGATGACAGGGTTAAAGGCTCTGGAATCTCAAAAATTTGTTT 490  
Qy 221 AGAAGTAATGAATAGGATGATTTACCTGACTGATTTGCTGGAAGAGCTTAGGGAAGTGA 280  
Db 491 AGAAGTAATGAATAGGATGATTTACCTGACTGATTTGCTGGAAGAGCTTAGGGAAGTGA 550  
Qy 281 TTCCAGGTCCTCAGCACCAAGACACACCCGTTTACCTGGGAGCCAGGCAAGGATGCGGT 340  
Db 551 TTCCAGGTCCTCAGCACCAAGACACACCCGTTTACCTGGGAGCCAGGCAAGGATGCGGT 610  
Qy 341 TGCTCAGGATGGAAGATGAAGATTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGCC 400  
Db 611 TGCTCAGGATGGAAGATGAAGATTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGCC 670

RESULT 9  
US-10-240-965-242  
; Sequence 242, Application US/10240965  
; Publication No. US20030165924A1

Qy 401 TCAGCAATACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCCCAAGAGGAGTG 640  
Db 671 TCAGCAATACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCCCAAGAGGAGTG 730  
Qy 461 CTTATGGCTGGATTAATACTAACTATCTGCTGGGCAAAATTCAGTCAAGAAAAAAGGTGGT 520  
Db 731 CTTATGGCTGGATTAATACTAACTATCTGCTGGGCAAAATTCAGTCAAGAAAAAAGGTGGT 790  
Qy 521 TCAGCATAGTCCCATATGAAACCAATATCAGGAACCACTTTTGGAGCTTTGGACCTTTGGGG 580  
Db 791 TCAGCATAGTCCCATATGAAACCAATATCAGGAACCACTTTTGGAGCTTTGGACCTTTGGGG 850  
Qy 581 GAGCCTCTACACAAGTCACTTTTGTATCCCAAAAACAGACTATCGAGTCCCAGATAATG 640  
Db 851 GAGCCTCTACACAAGTCACTTTTGTATCCCAAAAACAGACTATCGAGTCCCAGATAATG 910  
Qy 641 CTTCTCAATTTTCGCTCTATATGGCAAGGACTACAATGTCTTACACATAGTCTTCTGTGCT 700  
Db 911 CTTCTCAATTTTCGCTCTATATGGCAAGGACTACAATGTCTTACACATAGTCTTCTGTGCT 970  
Qy 701 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 760  
Db 971 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 1030  
Qy 761 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAGTACC 820  
Db 1031 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAGTACC 1090  
Qy 821 TTTTACAAGACCCCTTGCAACAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 880  
Db 1091 TTTTACAAGACCCCTTGCAACAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1150  
Qy 881 TCCAGGGTATTGGAAACTATCAACATGCCATCAAGGATCCTGGAGCTCTTCAACACCA 940  
Db 1151 TCCAGGGTATTGGAAACTATCAACATGCCATCAAGGATCCTGGAGCTCTTCAACACCA 1210  
Qy 941 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCACCACCTCCAGGGG 1000  
Db 1211 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCACCACCTCCAGGGG 1270  
Qy 1001 ATTTTGGGCAATTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1060  
Db 1271 ATTTTGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1330  
Qy 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATCAAAAAGTTCTGTGCTCAGCCTTGGGAGG 1120  
Db 1331 AAGTCTCTCAGGAAAGGTGACTGAGATGATCAAAAAGTTCTGTGCTCAGCCTTGGGAGG 1390  
Qy 1121 AGATAAAAACATCTTACCGTGGAGTAAAGGAAAGTACCTGAGTGAATACTGCTTTTCTG 1180  
Db 1391 AGATAAAAACATCTTACCGTGGAGTAAAGGAAAGTACCTGAGTGAATACTGCTTTTCTG 1450  
Qy 1181 GTACCTTACATTTCTCCCTCTTCTGCAAGGCTATCATTTTTCAGCTGATTTCTTGGGAGC 1240  
Db 1451 GTACCTTACATTTCTCCCTCTTCTGCAAGGCTATCATTTTTCAGCTGATTTCTTGGGAGC 1510  
Qy 1241 ACATCCATTTTCTTGGCAGATCCAGGCGAGCGCGGCTGGACTTTTGGGCTACATGC 1300  
Db 1511 ACATCCATTTTCTTGGCAGATCCAGGCGAGCGCGGCTGGACTTTTGGGCTACATGC 1570  
Qy 1301 TGAACCTGACCAACATGATCCCAGCTGAGCAACCAATTTGTCCACACCTCTCTCCCACTCCA 1360  
Db 1571 TGAACCTGACCAACATGATCCCAGCTGAGCAACCAATTTGTCCACACCTCTCTCCCACTCCA 1630  
Qy 1361 CCTA 1364  
Db 1631 CCTA 1634



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GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SHIFFMAN, Dov
APPLICANT: SOMOGYI, Roland
APPLICANT: LAWN, Richard M.
APPLICANT: SEILHAMER, Jeffrey J.
APPLICANT: PORTER, Gordon J.
APPLICANT: MIKITA, Thomas
APPLICANT: TAI, Julie
TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
FILE REFERENCE: PA-0025 PCT
CURRENT APPLICATION NUMBER: US/10/240,965
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 276
SOFTWARE: PERL Program
SEQ ID NO 242
LENGTH: 4411
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030165924A1 347965.2
FEATURE:
NAME/KEY: unsure
LOCATION: 3369
OTHER INFORMATION: a, t, c, g, or other
US-10-240-965-242

```

Query Match	96.6%;	Score 1319.2;	DB 16;	Length 4411;	
Best Local Similarity	99.8%;	Pred. No. 0;			
Matches 1321;	Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	41	GTTCAACCCAGAACAAAGCATTTGCCAGAAAAAGTTTAAGTATGGGATTTGCTGCGATCGG	100		
Db	184	GTTGACCCAGAACAAAGCATTTGCCAGAAAAGTTTAAGTATGGGATTTGCTGCGATCGG	243		
QY	101	GTTCTTCTCACAAAGTTTATACATCTTATAAGTGGCCAGCAGAAAAAGAGAAATGACACAG	160		
Db	244	GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGAGAAATGACACAG	303		
QY	161	CGGTGGTCATCAGTAGAAGATGACAGGTTTAAAGTCTCTGGAAATCTCAAAAATTTGTTTC	220		
Db	304	CGGTGGTCATCAGTAGAAGATGACAGGTTTAAAGTCTCTGGAAATCTCAAAAATTTGTTTC	363		
QY	221	AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTTGCATCGAAAGAGCTAGGGAAGTGA	280		
Db	364	AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTTGCATCGAAAGAGCTAGGGAAGTGA	423		
QY	281	TTCCAAGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGGCCACGGCAGGCAATGCGGT	340		
Db	424	TTCCAAGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGGCCACGGCAGGCAATGCGGT	483		
QY	341	TGCTCAGAGTGGAAAGTCAAGAGTTGGCAGACAGGGTTCTGGATGCTGGAGAGGAGCC	400		
Db	484	TGCTCAGAGTGGAAAGTCAAGAGTTGGCAGACAGGGTTCTGGATGCTGGAGAGGAGCC	543		
QY	401	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGGGCCAAGAGGAAGTG	460		
Db	544	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGGGCCAAGAGGAAGTG	603		
QY	461	CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTTCAGAAAACAAGTGGT	520		
Db	604	CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTTCAGAAAACAAGTGGT	663		
QY	521	TCAGCATAGTCCCATATGAAACCAATATCAGGAAAACCTTTGGAGCTTTTGGACCTTCGGG	580		
Db	664	TCAGCATAGTCCCATATGAAACCAATATCAGGAAAACCTTTGGAGCTTTTGGACCTTCGGG	723		
QY	581	GAGCCTCTACAAAGTCACTTTTGTACCCCAAAAACCGACTATTCGAGTCCCCAGATAATG	640		
Db	724	GAGCCTCTACAAAGTCACTTTTGTACCCCAAAAACCGACTATTCGAGTCCCCAGATAATG	783		

RESULT 10  
US-10-934  
; Sequences  
; Publications  
; GENERAL  
; APPLIC  
; APPLIC  
; APPLIC  
; TITLE  
; TITLE  
; FILE RE  
; CURRENT  
; PRIOR  
; PRIOR  
; PRIOR  
; PRIOR  
; PRIOR

RESULT 10  
US-10-934-998-147/c  
; Sequence 147, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11

```

; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 147
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-934-998-147

Query Match      46.9%; Score 640.2; DB 22; Length 704;
Best Local Similarity 99.5%; Pred. No. 4.3e-193;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 720 CTGCGAGAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGACCCCATG 779
Db 704 CTGCGAGAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGACCCCATG 645

Qy 780 CTTTTCATCTCGATATATAAGAAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCAC 839
Db 644 CTTTTCATCTCGATATATAAGAAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCAC 585

Qy 840 CAAGAGATTGAGATGACTCTTCATTCAGCATCCAGCAGTTTGAATCCAGGGTATTGGAAACTA 899
Db 584 CAAGAGATTGAGATGACTCTTCATTCAGCATCCAGCAGTTTGAATCCAGGGTATTGGAAACTA 525

Qy 900 TCAACAATGCCATCAAGCATCTGGAGCTCTTCAACACAGTTACTTGCCCTTACTCCCA 959
Db 524 TCAACAATGCCATCAAGCATCTGGAGCTCTTCAACACAGTTACTTGCCCTTACTCCCA 465

Qy 960 GTGTGCCCTTCAATGGGATTTTCTTGCCACCCTCCAGGGGATTTTGGGGCAATTTTCAGC 1019
Db 464 GTGTGCCCTTCAATGGGATTTTCTTGCCACCCTCCAGGGGATTTTGGGGCAATTTTCAGC 405

Qy 1020 TTTTACTTTGTGATGAAGTTTAACTTGATCAGAGAAAGTCTCTCAGGAAAAGGT 1079
Db 404 TTTTACTTTGTGATGAAGTTTAACTTGATCAGAGAAAGTCTCTCAGGAAAAGGT 345

Qy 1080 GACTGAGATCATGAAGAAGTTCTGTCTCAGCCTCGGGAGAGATAAAACATCTTACGC 1139
Db 344 GACTGAGATCATGAAGAAGTTCTGTCTCAGCCTCGGGAGAGATAAAACATCTTACGC 285

Qy 1140 TGGAGTAAAGGAGAACTGCTGAGTGAATACTGCTTTCTGTGTACCTACATTTCTCCCT 1199
Db 284 TGGAGTAAAGGAGAACTGCTGAGTGAATACTGCTTTCTGTGTACCTACATTTCTCCCT 225

Qy 1200 CCTTCTGCAAGGCTATCTTTCAGCTGATTTCTGAGGACATCGATTTTCAATGGCAA 1259
Db 224 CCTTCTGCAAGGCTATCTTTCAGCTGATTTCTGAGGACATCGATTTTCAATGGCAA 165

Qy 1260 GATCCAGGCGAGCAGCGCGCTGGACTTTTGGGCTACATGCTGAACCTGACCAACATGAT 1319
Db 164 GATCCAGGCGAGCAGCGCGCTGGACTTTTGGGCTACATGCTGAACCTGACCAACATGAT 105

Qy 1320 CCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCACCTA 1364
Db 104 CCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCACCTA 60
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RESULT 11
US-10-934-998-193/c
; Sequence 193, Application US/10934998
; Publication No. US20050153917A1
; GENERAL INFORMATION:
; APPLICANT: AL-WAHMOOD, SALMAN
; APPLICANT: COLIN, SYLVIE
; APPLICANT: SCHNEIDER, CHRISTOPHE
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
; TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
; FILE REFERENCE: BNA-04-1206
; CURRENT APPLICATION NUMBER: US/10/934, 998
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/FR03/00695
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: FR02/02717
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; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR02/04546
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193
; LENGTH: 6164
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-934-998-193

Query Match      46.9%; Score 640.2; DB 22; Length 6164;
Best Local Similarity 99.5%; Pred. No. 1.6e-192;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 720 CTGCGAGAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGACCCCATG 779
Db 1811 CTGCGAGAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGACCCCATG 1752

Qy 780 CTTTTCATCTCGATATATAAGAAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCAC 839
Db 1751 CTTTTCATCTCGATATATAAGAAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCAC 1692

Qy 840 CAAGAGATTGAGATGACTCTTCCATTCAGCAGATTTTGAATCCAGGGTATTGGAAACTA 899
Db 1691 CAAGAGATTGAGATGACTCTTCCATTCAGCAGATTTTGAATCCAGGGTATTGGAAACTA 1632

Qy 900 TCAACAATGCCATCAAGCATCTGGAGCTCTTCAACACAGTTACTTGCCCTTACTCCCA 959
Db 1631 TCAACAATGCCATCAAGCATCTGGAGCTCTTCAACACAGTTACTTGCCCTTACTCCCA 1572

Qy 960 GTGTGCCCTTCAATGGGATTTTCTTGCCACCCTCCAGGGGATTTTGGGGCAATTTTCAGC 1019
Db 1571 GTGTGCCCTTCAATGGGATTTTCTTGCCACCCTCCAGGGGATTTTGGGGCAATTTTCAGC 1512

Qy 1020 TTTTACTTTGTGATGAAGTTTAACTTGATCAGAGAAAGTCTCTCAGGAAAAGGT 1079
Db 1511 TTTTACTTTGTGATGAAGTTTAACTTGATCAGAGAAAGTCTCTCAGGAAAAGGT 1452

Qy 1080 GACTGAGATGAAGAAAGTTCTGTCTCAGCCTTGGGAGAGATAAAACATCTTACGC 1139
Db 1451 GACTGAGATGAAGAAAGTTCTGTCTCAGCCTTGGGAGAGATAAAACATCTTACGC 1392

Qy 1140 TGGAGTAAAGGAGAACTGCTGAGTGAATACTGCTTTCTGTGTACCTACATTTCTCCCT 1199
Db 1391 TGGAGTAAAGGAGAACTGCTGAGTGAATACTGCTTTCTGTGTACCTACATTTCTCCCT 1332

Qy 1200 CCTTCTGCAAGGCTATCTTTCAGCTGATTTCTGAGGACATCCATTTTCAATGGCAA 1259
Db 1331 CCTTCTGCAAGGCTATCTTTCAGCTGATTTCTGAGGACATCCATTTTCAATGGCAA 1272

Qy 1260 GATCCAGGCGAGCAGCGCGCTGGACTTTTGGGCTACATGCTGAACCTGACCAACATGAT 1319
Db 1271 GATCCAGGCGAGCAGCGCGCTGGACTTTTGGGCTACATGCTGAACCTGACCAACATGAT 1212

Qy 1320 CCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCACCTA 1364
Db 1211 CCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCACCTA 1167
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RESULT 12
US-09-918-995-24656
; Sequence 24656, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
```

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; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24656
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-24656

Query Match      30.3%; Score 414; DB 10; Length 475;
Best Local Similarity 96.6%; Pred. No. 6.3e-121;
Matches 423; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 593 AAGTCACTTTGTACCCCAAAACAGACTATCCAGTCCCGAGATAATGCTCTGCAATTC 552
Db 38 AGGGCACTTATGATACCCCTTAACAGACTATCCAGTCCCGAGATAATGCTCTGCAATTC 97
QY 653 GCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGCTATGGGAAGATC 712
Db 98 ACCTCTATGGCAGGACTACATGTCTACACATAGCTTCTTGCTATGGGAAGATC 157
QY 713 AGGCACCTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCCAAGTAATGAAATTC 772
Db 158 ATGCACCTCTGGCATAAATCGGCAAGGACATTCAGGTTGCAAGTAATGAAATTC 217
QY 773 ACCCATGCTTTCATCTCGATATAGAAGTAGTGAAGTGAAGTGAAGTGAAGTGAAG 832
Db 218 ACCCATGCTTTCATCTCGATATAGAAGTAGTGAAGTGAAGTGAAGTGAAGTGAAG 277
QY 833 CTGCAACCAAGAGATTGAGATGACTCTCCATTCAGAGATTTGAAATCCAGGGTATG 892
Db 278 CTGCAACCAAGAGATTGAGATGACTCTCCATTCAGAGATTTGAAATCCAGGGTATG 337
QY 893 GAAACTATCAACAATGCCATCAAGGATCTCGAGCTCTTCAACACAGTTACTGCGCTT 952
Db 338 GAAACTATCATCAATGCCATCAAGGATCTCGAGCTCTTCAACACAGTTACTGCGCTT 397
QY 953 ACTCCAGTGTGCTTCAATGGGATTTCTTGCCACACTCCAGGGGATTTTGGGGCAT 1012
Db 398 ACTCCAGTGTGCTTCAATGGGATTTCTTGCCACACTCCAGGGGATTTTGGGGCAT 457
QY 1013 TTTTCAGCTTTTACTTTG 1030
Db 458 TTTTCAGCTTTTACTTTG 475

RESULT 13
US-09-918-995-23052
; Sequence 23052, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23052
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(484)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-23052

Query Match      27.8%; Score 379; DB 10; Length 484;
Best Local Similarity 100.0%; Pred. No. 9.8e-110;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 986 CACCACTCCAGGGGATTTTGGGCAATTTTTCAGCTTTTTCATTTTGTGATGAAGTTTTTAA 1045
Db 50 CACCACTCCAGGGGATTTTGGGCAATTTTTCAGCTTTTTCATTTTGTGATGAAGTTTTTAA 109
QY 1045 ACTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGATGATGATGATGATGATGATGATG 1105
Db 110 ACTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGATGATGATGATGATGATGATGATG 169
QY 1106 CTCAGCCTTGGGAGGAGATATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACTCGAGTG 1165
Db 170 CTCAGCCTTGGGAGGAGATATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACTCGAGTG 229
QY 1166 AATATGCTTTTCTGCTACCTACATTTCTCTCCCTCTCTCTCAAGGCTATCATTTTCACAG 1225
Db 230 AATATGCTTTTCTGCTACCTACATTTCTCTCCCTCTCTCTCAAGGCTATCATTTTCACAG 289
QY 1226 CTGATTCCTGGGAGGACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGGCTGGA 1285
Db 290 CTGATTCCTGGGAGGACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGGCTGGA 349
QY 1286 CTTTGGGCTTACATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACAC 1345
Db 350 CTTTGGGCTTACATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACAC 409
QY 1346 CTCTCTCCCACTCCACCTA 1364
Db 410 CTCTCTCCCACTCCACCTA 428

RESULT 14
US-10-002-631C-275/c
; Sequence 275, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
; CURRENT APPLICATION NUMBER: US/10/002,631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275
; LENGTH: 703
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (656)...(698)
; OTHER INFORMATION: n = A, C, G, or T
US-10-002-631C-275

Query Match      24.6%; Score 335.8; DB 16; Length 703;
Best Local Similarity 80.2%; Pred. No. 7.8e-96;
Matches 394; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 46 ACCCAGAACAAAGCATTTCCGAGAAACCGTTAAGTATGGGATTTGCTGATCGGGTTCT 105
Db 547 ACCCAGAACAAACCTTTTCCGAGAAATGTTAAGTATGGGATTTGCTGATCGGGGTCA 488
QY 106 TCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAGAAAAGGAGAAATGACACAGCGTG 165
Db 487 TCTCACACAACCTGTTATCTCTACAAGTGGCCGCGCCGAGAGAGAAATGACACAGCGTG 428
QY 166 GTGCATCAAGTAGAAGAAATGAGGCTTAAAGGTTCTCGAAATCTCAAAATTTGTTTCAGAAA 225
Db 427 GTGCAGCAGTTAGAGGAATGCAAGTGAAGAGTCTCTGGAATCTCAAAATATGCTCAGAAA 368
QY 226 GTAATGAATAGGCAATTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGAATCCA 285
```

Db 367 ACAGATCAAAATCGGTACCTGGCCGCAATGATGCAAGTCTCCACCGAAGTATACCA 308  
 Qy 286 AGTCCAGCACCAGAGACACCCGTTTACCTGGGAGCCACGCGCAGGATGCGGTTGCTC 345  
 Db 307 ACATCAAGCATCACAGACTCCTGCTTACCTGGAGCCACAGCAGCATGCGCTTGCCTT 248  
 Qy 346 AGATGGAAAGTGAAGATGGCAGACAGGTTCTGATGCTGGATGGTGGAGGAGCCTCAGC 405  
 Db 247 AGAATGGAAAGCGAACAATCGGAGAGAGGTTCTGGCTGCAATGCAACAAGCCCTTAAG 188  
 Qy 406 AACTACCCCTTTGACTTCCAGGGTGCAGGATCAATTAAGTCCCAAGAGGAAGTGCCTAT 465  
 Db 187 AGCTACCCCTTTGACTTCCAGGGTGCAGGATCAATTAAGTCCCAAGAGGAAGTGCCTAT 128  
 Qy 466 GGCTGGAATTAATCAACTATCTGCTGGGCAAAATTCAGTCCAGAAAAACAAGTGGTTCAGC 525  
 Db 127 GGGTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 68  
 Qy 526 ATAGTCCCAT 536  
 Db 67 CTATCTCAGA 57

RESULT 15  
 US-09-923-304-3  
 ; Sequence 3, Application US/09923304  
 ; Patent No. US20020081612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KATZ, RUTH  
 ; APPLICANT: JIANG, FENG  
 ; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS  
 ; FILE REFERENCE: UTSC:658US  
 ; CURRENT APPLICATION NUMBER: US/09/923,304  
 ; CURRENT FILING DATE: 2001-08-06  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 2797  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (83)..(1672)  
 ; US-09-923-304-3

Query Match 21.3%; Score 291; DB 9; Length 2797;  
 Best Local Similarity 54.3%; Pred. No. 3.7e-81;  
 Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

Qy 48 CCAGAACAAAGCATGGCCAGAAACGTTAAGTATGGATGTTGCTGGATGCGGGTCTTTC 107  
 Db 220 CAAGCAAGAGGTCTCCCTCCAGGACTGAAAGTATGTTGCTGGATGCGGGTCTTTC 279  
 Qy 108 TCACACAAGTTTATACATCTAATGTCGCCAGAGAAAGAGAAATGACACAGCGCTGGT 167  
 Db 280 AAGAACCAAGTCTACGTGATCAATGGCCAGAGAAAGAGAAATTAATCCGAGTGGT 339  
 Qy 168 GCATCAAGTAGAAGATGACAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTCAGAAAGT 227  
 Db 340 CAGTCAAACTTCAAAATGTAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAAACC 399  
 Qy 228 AATGAATAGGATTTACCTGACTGATTCATGTCGAGGAGGATGAGGAGTGAATTCAG 287  
 Db 400 CCAAGATGTCCCGAGAGCCTTTGAGGAGTGTATGCAAAAAGTCAAGGGGAGGCTCCATC 459  
 Qy 288 GTCCAGCACAGAGACACCCGTTTACCTGGGAGCCAGCGAGGATGCGGTTGCTCAG 347  
 Db 460 CCACCTCCAGGATCCACCCCAATTCACCTGGGAGCCAGCGCTGGGATGCGCTTGTGAG 519  
 Qy 348 GATGGAAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTTGGTGGAGAGGAGCCTCAGCAA 407  
 Db 520 GTTGCAAAATGAACAGCAGCCTAATGAAGTCTTTGAAAGCATCCAAAGCTACTTCAAGTC 579

Search completed: September 22, 2005, 04:37:21  
 Job time : 993.919 secs

Qy 408 CTACCCCTTTGACTTCCAGGGTCCAGGATCAATTAAGTCCCAAGAGGAAGTGCCTATGG 467  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 16:22:35 ; Search time 6446.5 Seconds  
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10801.234 Million cell updates/sec

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Perfect score: 1437

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Scoring table:

IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1437	100.0	1437	6	BD228700 Inhibitor
2	1400	97.4	1464	6	BD228710 Inhibitor
3	1365	95.0	1365	6	BD228699 Inhibitor
4	1319.2	91.8	1599	6	BD228698 Inhibitor
5	1319.2	91.8	1704	9	HSU87967 Human ATP d
6	1319.2	91.8	1818	6	AR168353 Sequence
7	1319.2	91.8	1818	6	AR380930 Sequence
8	1319.2	91.8	1818	6	AX828644 Sequence
9	1319.2	91.8	1818	9	S73813 CD39=lympho
10	1319.2	91.8	2081	6	AX828400 Sequence
11	1319.2	91.8	2081	9	HSAL133133 Homo sapi
12	1319.2	91.8	2986	6	CQ870272 Sequence
13	1319.2	91.8	3236	6	CQ870276 Sequence
14	1319.2	91.8	3502	6	CQ870270 Sequence
15	1319.2	91.8	4411	6	AX281833 Sequence
16	1305.2	90.8	3506	6	CQ870274 Sequence
17	1039	72.3	1479	6	CQ769356 Sequence
18	1019.8	71.0	1665	9	BC047664 Homo sapi
19	888.4	61.8	1648	4	SSC133746 Sus scrofa

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21	863	60.1	2386	10	BC011278	BC011278 Mus muscu
22	858.2	59.7	1686	10	RNU81295	U81295 Rattus norv
23	835	58.1	2296	6	CQ870265	Sequence
24	827.8	57.6	1958	4	AF005940	AF005940 Bos tauru
25	703.2	48.9	1488	6	CQ870268	Sequence
26	703.2	48.9	1815	9	HSAL133134	HSAL133134 Homo sapi
c 27	640.2	44.6	704	6	AX828501	Sequence
c 28	640.2	44.6	6164	6	AX828547	Sequence
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30	524.4	36.5	3211	5	BC076662	BC076662 Xenopus t
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37	291	20.3	2797	6	AR567207	AR567207 Sequence
38	291	20.3	2797	6	AR567913	AR567913 Sequence
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ALIGNMENTS

BD228700 1437 bp DNA linear PAT 17-JUL-2003  
Inhibitors of platelet activation and recruitment.  
BD228700.1 GI:33038470  
JP 2002527096-A/3.  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
i (bases 1 to 1437)  
Maliszewski, C.R., Ili, R.B.G., Price, V.L. and Gimpe, S.D.  
Inhibitors of platelet activation and recruitment  
Patent: JP 2002527096-A 3 27-AUG-2002;  
IMMUNEX CORP  
OS Artificial Sequence  
PN JP 2002527096-A/3  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185  
PR 16-OCT-1998 US 60/104585,06-NOV-1998 US 60/107466 PR  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI  
STEVEN D GIMPEL  
PC C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC  
C12N5/10,  
PC C12P21/02, C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC  
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FH Key Location/Qualifiers  
FT CDS  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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61	Db	 GTCACAACAGTGCACCTACTTCAAGTTCTACAAAGAAACACACAGCTAACTAGTTCGAACC	120
121	Qy	 CAGAAACAAAGCATTTGCCAGAAAACGTTTAAGTATGGGATTTGTGTGGATGCGGGTCTTCT	180
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LOCUS	BD228710	1464 bp	DNA linear
DEFINITION	Inhibitors of platelet activation and recruitment.		
ACCESSION	BD228710		
VERSION	BD228710.1	GI:33038480	
KEYWORDS	JP 2002527096-A/13.		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1 (bases 1 to 1464)		
AUTHORS	Maliszewski,C.R., Iii,R.B.G., Price,V.L. and Gimpe,S.D.		
TITLE	Inhibitors of platelet activation and recruitment		
JOURNAL	Patent: JP 2002527096-A 13 27-AUG-2002;		
COMMENT	IMMUNEX CORP		
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	PN JP 2002527096-A/13		
	PD 27-AUG-2002		
	PF 13-OCT-1999 JP 2000577185		
	PR 16-OCT-1998 US 60/104585,06-NOV-1998 US 60/107466 PR		
	13-AUG-1999 US 60/149010		
	PI CHARLES R MALISZEWSKI,RICHARD B GAYLE III,VIRGINIA L PRICE,PI		
	PC C12N15/09,A61K38/00,A61P9/00,C07K14/705,C12N1/15,C12N1/19,PC		
	C12N5/10,		
	PC C12P21/02//C12N9/14,C12N15/00,A61K37/02,C12N5/00 CC		
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DEFINITION Inhibitors of platelet activation and recruitment.  
ACCESSION BD228699  
VERSION JP 2002527096-A/2.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 1365)  
AUTHORS Maliszewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D.  
TITLE Inhibitors of platelet activation and recruitment  
JOURNAL Patent: JP 2002527096-A 2 27-AUG-2002;  
IMMUNEX CORP  
COMMENT OS Artificial Sequence  
PN JP 2002527096-A/2  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185 60/104585,06-NOV-1998 US 60/107466 PR  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI  
STEVEN D GIMPEL  
PC C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC  
C12N5/10,  
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Description of Artificial Sequence: Fusion construct of human CC  
CD39

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Kaczmarek,E., Koziak,K., Sevigny,J., Siegel,J.B., Anrather,J.,  
Beaudoin,A.R., Bach,F.H. and Robson,S.C.  
Identification and characterization of CD39/vascular ATP  
diphosphohydrolase  
J. Biol. Chem. 271 (51), 33116-33122 (1996)  
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2 (bases 1 to 1704)  
Robson,S.C., Kaczmarek,E., Siegel,J.B., Candinas,D., Koziak,K.,  
Millan,M., Hancock,W.W. and Bach,F.H.  
Loss of ATP diphosphohydrolase activity with endothelial cell  
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J. Exp. Med. 185 (1), 153-163 (1997)  
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Kaczmarek,E., Koziak,K., Sevigny,J., Siegel,J.B., Anrather,J.,  
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Qy	1253	GTACTACATTTCTCTCCCTCTCTCTGCAAGGCTATCATTTCAACAGCTGATTCCTGGGAGC	1312						
Db	1314	GTACTACATTTCTCTCCCTCTCTCTGCAAGGCTATCATTTCAACAGCTGATTCCTGGGAGC	1373						
Qy	1313	ACATCCATTTTCAATGGCAAGATCCAGGCAAGGACGCGCGGTGAGCTTTGGGCTACATGC	1372						
Db	1374	ACATCCATTTTCAATGGCAAGATCCAGGCAAGGACGCGCGGTGAGCTTTGGGCTACATGC	1433						
Qy	1373	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCCCACTCCA	1432						
Db	1434	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCCCACTCCA	1493						
Qy	1433	CCTA 1436							
Db	1494	CCTA 1497							
RESULT 7									
LOCUS	AR380930	1818 bp	DNA linear PAT 18-DEC-2003						
DEFINITION	Sequence 1475 from patent US 6607879.								
ACCESSION	AR380930								
VERSION	AR380930.1 GI:40088564								
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 1818)								
AUTHORS	Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.								
TITLE	Compositions for the detection of blood cell and immunological								
JOURNAL	response gene expression								
FEATURES	Patent: US 6607879-A 1475 19-AUG-2003;								
source	Location/Qualifiers								
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Query Match	91.8%;	Score 1319.2;	DB 6; Length 1818;						
Best Local Similarity	99.8%;	Pred. No. 0;							

Query Match 91.8%; Score 1319.2; DB 6; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;

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QY 1253 GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTTACAGCTGATTTCTCGGAGC 1312  
Db 1314 GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTTACAGCTGATTTCTCGGAGC 1373  
QY 1313 ACATCCATTTTCTGGAAGATCCAGGCGAGCGAGCGCGGCTGGACTTTGGGCTACATGC 1372  
Db 1374 ACATCCATTTTCTGGAAGATCCAGGCGAGCGAGCGCGGCTGGACTTTGGGCTACATGC 1433  
QY 1373 TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1432  
Db 1434 TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1493  
QY 1433 CCTA 1436  
Db 1494 CCTA 1497

RESULT 8  
AX828644  
LOCUS  
DEFINITION Sequence 290 from Patent WO03074073.  
ACCESSION AX828644  
VERSION AX828644.1 GI:39838595  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Al-Mahmood,S., Colin,S. and Schneider,C.  
Genes involved in regulating angiogenesis, pharmaceutical  
preparations containing same and applications thereof  
Patent: WO 03074073-A 290 12-SEP-2003;  
JOURNAL  
Gene Signal (FR)  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 91.8%; Score 1319.2; DB 6; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 113 GTTCAACCCAGAACAAAGCATTCGCAGAAACGTTAAGTATGGATTTGCTGGATCGG 172  
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QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAGGAGAATGACACAG 232  
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAGGAGAATGACACAG 293  
QY 233 GCGTGGTGCA TCAAGTAGAAGAAATGCAAGGTTAAAGTCTCGAAATCTCAAAAATTTGTTTC 292  
Db 294 GCGTGGTGCA TCAAGTAGAAGAAATGCAAGGTTAAAGTCTCGAAATCTCAAAAATTTGTTTC 353  
QY 293 AGAAAGTAAATGAAATAGGCAATTTACTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 352  
Db 354 AGAAAGTAAATGAAATAGGCAATTTACTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 413  
QY 353 TTCCAGGTCCTCCAGCACCAAGAGACACCCCTTTTACCTGGGAGCCAGCGGAGCATCGGT 412  
Db 414 TTCCAGGTCCTCCAGCACCAAGAGACACCCCTTTTACCTGGGAGCCAGCGGAGCATCGGT 473  
QY 413 TGCTCAGGATGGAAGTAGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 472  
Db 474 TGCTCAGGATGGAAGTAGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 533

RESULT 9  
S73813  
LOCUS

S73813 1818 bp mRNA linear PRI 12-APR-1995

QY 473 TCAGCAACTACCCCTTTTGACTTCCAGGTTGCCAGGATCATTTACTGGCCCAAGAGGAGTG 532  
Db 534 TCAGCAACTACCCCTTTTGACTTCCAGGTTGCCAGGATCATTTACTGGCCCAAGAGGAGTG 593  
QY 533 CCTATGGCTGGATTAATACTCAATCTCTCTGGGCAAAATTCAGTCAGAAAAAAGGTGGT 592  
Db 594 CCTATGGCTGGATTAATACTCAATCTCTCTGGGCAAAATTCAGTCAGAAAAAAGGTGGT 653  
QY 593 TCAGCATAGTCCCATATGAACCAATATCAGGAAACCTTTTGGAGCTTTGGACCTTGGGG 652  
Db 654 TCAGCATAGTCCCATATGAACCAATATCAGGAAACCTTTTGGAGCTTTGGACCTTGGGG 713  
QY 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
Db 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 773  
QY 713 CTCTCAATTTTCGCCTCTATGGCAAGGACTACAATGTCTTACACATAGCTTCTTGTGCT 772  
Db 774 CTCTCAATTTTCGCCTCTATGGCAAGGACTACAATGTCTTACACATAGCTTCTTGTGCT 833  
QY 773 ATGGGAAGGATCAGGCACTCTGGCAAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832  
Db 834 ATGGGAAGGATCAGGCACTCTGGCAAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893  
QY 833 AATTTCTCAGGACCCCATGCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAAGTACC 892  
Db 894 AATTTCTCAGGACCCCATGCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAAGTACC 953  
QY 893 TTTTACAAGACCCCTGCAACAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 952  
Db 954 TTTTACAAGACCCCTGCAACAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 1013  
QY 953 TCAGGATTTTGGAAACTATCAAAATGCCATCAAGCATCTCTGGAGCTTTCAACACCA 1012  
Db 1014 TCAGGATTTTGGAAACTATCAAAATGCCATCAAGCATCTCTGGAGCTTTCAACACCA 1073  
QY 1013 GTTACTGCCCTTACTTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCATCTCCAGGGG 1072  
Db 1074 GTTACTGCCCTTACTTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCATCTCCAGGGG 1133  
QY 1073 ATTTTGGGCAATTTTCACTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1132  
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QY 1133 AAGTCTCTCAGAAAGGAGTGAATGATGATAAGAAAGTTCTGTCTCAGCTTGGAGG 1192  
Db 1194 AAGTCTCTCAGAAAGGAGTGAATGATGATAAGAAAGTTCTGTCTCAGCTTGGAGG 1253  
QY 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1252  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1313  
QY 1253 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGAGC 1312  
Db 1314 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGAGC 1373  
QY 1313 ACATCCATTTTCTGGAAGATCCAGGCGAGCGAGCGCGGCTGGACTTTGGGCTACATGC 1372  
Db 1374 ACATCCATTTTCTGGAAGATCCAGGCGAGCGAGCGCGGCTGGACTTTGGGCTACATGC 1433  
QY 1373 TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1432  
Db 1434 TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1493  
QY 1433 CCTA 1436  
Db 1494 CCTA 1497

DEFINITION	CD39=lymphoid cell activation antigen [human, B lymphoblastoid cell line, MP-1, mRNA, 1818 nt].
ACCESSION	S73813
VERSION	S73813.1 GI:765255
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1818)
AUTHORS	Maliszewski, C.R., DeLesselee, G.J., Schoenborn, M.A., Armitage, R.J., Fanslow, W.C., Nakajima, T., Baker, E., Sutherland, G.R., Poindexter, K., Birks, C. et.al.
TITLE	The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization
JOURNAL	J. Immunol. 153 (8), 3574-3583 (1994)
MEDLINE	95015846
PUBMED	7930580
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbon 156681] from the original journal article.
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source	1..1818
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	/note="lymphoid cell activation antigen, CD39"
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Query Match	91.8%; Score 1319.2; DB 9; Length 1818;
Best Local Similarity	99.8%; Pred. No. 0;
Matches 1321; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Qy	113 GTTCAACCCAGAACATGCGCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGG 172
Db	174 GGTGACCCAGAACAAAGCATGCGCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGG 233
Qy	173 GTTCTTCTCACAAAGTTTATACATCTATAGTGGCCAGCAGAAAAGAGAAATGACACAG 232
Db	234 GTTCTTCTCACAAAGTTTATACATCTATAGTGGCCAGCAGAAAAGAGAAATGACACAG 293
Qy	233 CGGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGGTCCTGGAAATCTCAAAAATTTGTC 292
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Qy	293 AGAAAGTAAATGAATAGGCAATTTACCTGAGCTGATGCGATGCGAAGAGCTAGGGAAGTGA 352
Db	354 AGAAAGTAAATGAATAGGCAATTTACCTGAGCTGATGCGATGCGAAGAGCTAGGGAAGTGA 413
Qy	353 TTCAAAGGTCCAGCAGCAAGACACCCGTTTACCTGGGAGCCACGGCAGCATGCGGT 412
Db	414 TTCAAAGGTCCAGCAGCAAGACACCCGTTTACCTGGGAGCCACGGCAGCATGCGGT 473
Qy	413 TGCTCAGGATGGAAAGTAGAGAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGAGCC 472







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gene	
CDS	
ORIGIN	
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Qy	113 GTTCAACCCAGAACCAAGCAATTCAGCAAAACGTTAAAGTATGGGATTTGTCTGGATGCGG 172
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Qy	173 GTTCTTCTCACAAAGTTTATACATCTATAAGTGCCAGCAGAAAGAGAAATGACACAG 232
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Qy	233 GCGTGGTGCACTCAAGTAGAAGATCGAGGTTTAAAGTTCCTGGATCTCAAAATTTGTTTC 292
Db	431 GCGTGGTGCACTCAAGTAGAAGATCGAGGTTTAAAGTTCCTGGATCTCAAAATTTGTTTC 490
Qy	293 AGAAAGTAAATGAAATAGGCAATTTACCTGACTGATTTGCATGGAAGAGAGCTAGGGAAGTGA 352
Db	491 AGAAAGTAAATGAAATAGGCAATTTACCTGACTGATTTGCATGGAAGAGAGCTAGGGAAGTGA 550
Qy	353 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATGCGGT 412
Db	551 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATGCGGT 610
Qy	413 TGCTCAGATGGAAGAGTGAAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGCC 472
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Qy	473 TCAGCAACTACCCCTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCAACGAGGAAGGTG 532
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Qy	533 CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 592
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Qy	593 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 652
Db	791 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 850
Qy	653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACACAGACTATCAGTCCCCAGATAATG 712
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Qy	713 CTCTCAAAATTCGCCTCTATGCAAGGACTCAATGTCTACACACATAGCTTCTTGTGCT 772
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Qy	773 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGACATTCAGGTTGCAAGTAATG 832
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Qy	833 AAATTTCTCAGGAGCCCATGCTTTTCATCTCTGGATATAAGAAGGTAGTGAACGTAAGTGACC 892
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Qy	1013 GTTACTGCCCTTACTCTCCAGTGTCCTTCAATGGGATTTTCTTGCCACACACTCCAGGGGG 1072
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Qy	1073 ATTTTGGGGCAATTTTACGCTTTTACTTTGTGTAGTAAGTTTTTAAACTTGACATCAGAGA 1132
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Qy	1193 AGATAAAACATCTTACCGTGGAGTAAAGGAGAGTACTCTGAGTGAATACTGCTTTTCTG 1252
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Qy	1253 GTACTCATTTCTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGAGC 1312
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Qy	1313 ACATCCATTTTCTTGGCAAGATCCAGGACGCGGCTGGAGCTTTGGGCTACATGC 1372
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Qy	1373 TGAACCTTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1432
Db	1571 TGAACCTTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1630
Qy	1433 CCTA 1436
Db	1631 CCTA 1634
RESULT 12	
LOCUS	CQ870272 2986 bp DNA linear PAT 13-SEP-2004
DEFINITION	Sequence 693 from Patent WO2004/074320.
ACCESSION	CQ870272
VERSION	CQ870272.1 GI:51999878
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Morris, D.W., Morris, D.W. and Malandro, M.S.
TITLE	Novel therapeutic targets in cancer
JOURNAL	Patent: WO 2004/074320-A 693 02-SEP-2004;
	Sagres Discovery, Inc. (US)
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source	1. .2986
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Qy	173	GTTCCTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG	232						
Db	242	GTTCCTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG	301						
Qy	233	GCCTGTGCATCAAGTAGAAGAAATGACGGTTAAAGTCTCGGAATCTCAAAATTTGTTC	292						
Db	302	GCCTGTGTGATCAAGTAGAAGAAATGACGGTTAAAGTCTCGGAATCTCAAAATTTGTTC	361						
Qy	293	AGAAAGTAAATGAATAGGCATTTACTGACTGATTTGCAATGGAAAGAGCTAGGGAAGTGA	352						
Db	362	AGAAAGTAAATGAATAGGCATTTACTGACTGATTTGCAATGGAAAGAGCTAGGGAAGTGA	421						
Qy	353	TTCCAAAGGTCACAGCAACCAAGAGACACCCCGTTTACCTGGAGCCAGCGGCAATGCGGT	412						
Db	422	TTCCAAAGGTCACAGCAACCAAGAGACACCCCGTTTACCTGGAGCCAGCGGCAATGCGGT	481						
Qy	413	TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGCC	472						
Db	482	TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGCC	541						
Qy	473	TCAGCACTACCCCTTTGACTTCCAGGTGCGCAGGATCACTACTGCGCCAGAGGAGGTG	532						
Db	542	TCAGCACTACCCCTTTGACTTCCAGGTGCGCAGGATCACTACTGCGCCAGAGGAGGTG	601						
Qy	533	CCTATGGCTGGATTAATCAACTATCTGCTGGCCAAATTCAGTCAGAAAAACAAGTGGT	592						
Db	602	CCTATGGCTGGATTAATCAACTATCTGCTGGCCAAATTCAGTCAGAAAAACAAGTGGT	661						
Qy	593	TCAGCATAGTCCCATATGAACCAATAATCAGAAAAACCTTTGAGCTTTGGACCTTGGGG	652						
Db	662	TCAGCATAGTCCCATATGAACCAATAATCAGAAAAACCTTTGAGCTTTGGACCTTGGGG	721						
Qy	653	GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAAG	712						
Db	722	GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAAG	781						
Qy	713	CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT	772						
Db	782	CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT	841						
Qy	773	ATGGGAAGGATCAGGCATCTGCGAGAAACTGGCCAGGACATTCAGGTTGCAAGTAATG	832						
Db	842	ATGGGAAGGATCAGGCATCTGCGAGAAACTGGCCAGGACATTCAGGTTGCAAGTAATG	901						
Qy	833	AAATTTCTCAGGGACCCATGCTTTTCACTCTGGATATAAGAGGTAGTGAAGTAAAGTACC	892						
Db	902	AAATTTCTCAGGGACCCATGCTTTTCACTCTGGATATAAGAGGTAGTGAAGTAAAGTACC	961						
Qy	893	TTTACAAAGACCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA	952						
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Qy	953	TCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCGAGCTTCTCAACACCA	1012						
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Db	1142	ATTTTGGGGCATTTTACGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA	1201						
Qy	1133	AGTCTCTCAGGAAAGGTTGACTGAGATCATGAAAGAGTTCTGTGCTCAGCCTTTGGGAGG	1192						
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE 1									
MORRIS, D. W., MORRIS, D. W. and MALANDRO, M. S.									
Novel therapeutic targets in cancer									
Patent: WO 2004074320-A 697 02-SEP-2004;									
Sagres Discovery, Inc. (US)									
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ACCESSION CQ870270
VERSION CQ870270.1 GI:51999877
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS Morris,D.W., Morris,D.W. and Malandro,M.S.
TITLE Novel therapeutic targets in cancer
JOURNAL Patent: WO 2004074320-A 691 02-SEP-2004;
Sagres Discovery, Inc. (US)
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Best Local Similarity 99.8%; Pred. No. 0;
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Sequence 242 from Patent WO0177389.
ACCESSION
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VERSION
AX281833.1 GI:16609084
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SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,
Mikita,T. and Lai,J.
Genes expressed in foam cell differentiation
Patent: WO 0177389-A 242 18-OCT-2001;
Incyte Genomics, Inc. (US)
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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DT	17-AUG-2000 (first entry)
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KW	unstable angina; myocardial infarction; stroke; coronary artery disease;
KW	atherosclerosis; peripheral vascular occlusion; thromboclasia; embolism;
KW	platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW	coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW	thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW	antiangiinal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW	cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.
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OS	Synthetic.
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PF 13-OCT-1999; 99WO-US022955.  
XX  
PR 16-OCT-1998; 98US-0104585P.  
PR 06-NOV-1998; 98US-0107466P.  
PR 13-AUG-1999; 99US-0149010P.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;  
XX  
DR WPI; 2000-3339644/29.  
XX P-PSDB; AAY70914.  
XX  
DR New soluble CD39 polypeptides having apyrase activity, useful for  
PT inhibiting anglogenesis and treating unstable angina, myocardial  
PT infarction, stroke, coronary artery disease or injury.  
XX  
PS Claim 15a; Page 97-99; 122pp; English.  
XX  
CC The present DNA sequence is a fusion construct pIL2solCD39, comprising  
CC leader peptide of human interleukin 2 (hIL2), 12 amino acids from the  
CC mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region,  
CC having apyrase activity. This produces high levels of solCD39 expression  
CC and activity in the transfected cells. Soluble CD39 is constructed by  
CC removing the N- and C-terminal transmembrane domains. It retains the  
CC capacity to metabolise ATP and ADP at relevant concentrations and the  
CC ability to block and reverse ADP-induced platelet activation and  
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides  
CC are useful for inhibiting angiogenesis. It is useful for the treatment of  
CC unstable angina, myocardial infarction, stroke, coronary artery disease  
CC or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia,  
CC embolism, platelet-associated ischaemic disorders including lung,  
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,  
CC peripheral and cerebral artery thrombosis, intracardiac and venous  
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
CC stenosis or restenosis of blood vessels or stroke  
XX  
SQ Sequence 1437 BP; 411 A; 336 C; 335 G; 355 T; 0 U; 0 Other;

Query Match 100.0%; Score 1437; DB 3; Length 1437;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCCCTGTGGATCGACAGGATGCAACTCCTCTCTTGGATTGCACTAAAGTCTTGCACTT 60  
DB 1 ATGGCCCTGTGGATCGACAGGATGCAACTCCTCTCTTGGATTGCACTAAAGTCTTGCACTT 60  
QY 61 GTCACAAACAGTGCACCTACTTCAAGTTCTACAAAGAAACACAGCTTAAGTTCACAC 120  
DB 61 GTCACAAACAGTGCACCTACTTCAAGTTCTACAAAGAAACACAGCTTAAGTTCACAC 120  
QY 121 CAGAACAAAGCAATGCGAGAAACGTTAAGTATGGGATTTGCTGGATCGGGTCTTCT 180  
DB 121 CAGAACAAAGCAATGCGAGAAACGTTAAGTATGGGATTTGCTGGATCGGGTCTTCT 180  
QY 181 CACACAAGTTTATACATCTATAAGTGCCAGCAGAAAGAGAAATGACACAGCGTGGTG 240  
DB 181 CACACAAGTTTATACATCTATAAGTGCCAGCAGAAAGAGAAATGACACAGCGTGGTG 240  
QY 241 CATCAAGTAGAAGATGACGGGTTAAAGTCCCTGGATCTCAAAATTTGTTCAAGAAATA 300  
DB 241 CATCAAGTAGAAGATGACGGGTTAAAGTCCCTGGATCTCAAAATTTGTTCAAGAAATA 300  
QY 301 AATGAAATAGGCATTTACCTGACTGATTTGATGGAAGAGCTAGGGAAGTATTCCAAGG 360  
DB 301 AATGAAATAGGCATTTACCTGACTGATTTGATGGAAGAGCTAGGGAAGTATTCCAAGG 360  
QY 361 TCCAGCACCAAGAGACACCCGTTTACCTGGGACCAAGCGCATGCGGTTGCTCAGG 420  
DB 361 TCCAGCACCAAGAGACACCCGTTTACCTGGGACCAAGCGCATGCGGTTGCTCAGG 420

RESULT 2  
AAD00202  
ID AAD00202 standard; DNA; 1437 BP.  
XX

QY 421 ATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCTCAGCAAC 480  
DB |||||  
QY 421 ATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCTCAGCAAC 480  
DB |||||  
QY 481 TACCCCTTTTGACTTCCAGGGTCCAGGATCAATTAATCTGGCCAAAGAGAGGTCCTATGGC 540  
DB |||||  
QY 481 TACCCCTTTTGACTTCCAGGGTCCAGGATCAATTAATCTGGCCAAAGAGAGGTCCTATGGC 540  
DB |||||  
QY 541 TGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGTTCAGCATA 600  
DB |||||  
QY 541 TGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGTTCAGCATA 600  
DB |||||  
QY 601 GTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTGGGGGAGCCTCT 660  
DB |||||  
QY 601 GTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTGGGGGAGCCTCT 660  
DB |||||  
QY 661 ACACAAGTCACCTTTTGTATACCCCAAAACAGACTATCGAGTCCCCAGATTAATGCTCTGCAA 720  
DB |||||  
QY 661 ACACAAGTCACCTTTTGTATACCCCAAAACAGACTATCGAGTCCCCAGATTAATGCTCTGCAA 720  
DB |||||  
QY 721 TTTGCGCTCTATGGCAAGGACTACAAATGCTTACACACATAGCTTCTTGTGCTATGGGAAG 780  
DB |||||  
QY 721 TTTGCGCTCTATGGCAAGGACTACAAATGCTTACACACATAGCTTCTTGTGCTATGGGAAG 780  
DB |||||  
QY 781 GATCAGGCACTCTGCGCAGAAACCTGGCCAAAGGACATTCAGTTTGCAGAGTAATGAATTTCTC 840  
DB |||||  
QY 781 GATCAGGCACTCTGCGCAGAAACCTGGCCAAAGGACATTCAGTTTGCAGAGTAATGAATTTCTC 840  
DB |||||  
QY 841 AGGGACCCATGCTTTTCATCTCGATATAGAAGGTAGTGAACGTAAAGTCACTTTTACAAG 900  
DB |||||  
QY 841 AGGGACCCATGCTTTTCATCTCGATATAGAAGGTAGTGAACGTAAAGTCACTTTTACAAG 900  
DB |||||  
QY 901 ACCCCTGCAACAGAGATTGAGATGACTTCTTCCATCCAGCAGTTTCAAAATCCAGGCT 960  
DB |||||  
QY 901 ACCCCTGCAACAGAGATTGAGATGACTTCTTCCATCCAGCAGTTTCAAAATCCAGGCT 960  
DB |||||  
QY 961 ATTGGAACATCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCAAGTTACTGC 1020  
DB |||||  
QY 961 ATTGGAACATCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCAAGTTACTGC 1020  
DB |||||  
QY 1021 CTTTACTCCAGTGTCCCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGG 1080  
DB |||||  
QY 1021 CTTTACTCCAGTGTCCCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGG 1080  
DB |||||  
QY 1081 GCATTTTACGCTTTTACTTTTGTGATGAAGTTTAAACCTTCACATCAGAGAAAGTCTCT 1140  
DB |||||  
QY 1081 GCATTTTACGCTTTTACTTTTGTGATGAAGTTTAAACCTTCACATCAGAGAAAGTCTCT 1140  
DB |||||  
QY 1141 CAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGGAGATAAAA 1200  
DB |||||  
QY 1141 CAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGGAGATAAAA 1200  
DB |||||  
QY 1201 ACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATATCTGCTTTTCTGGTACCTAC 1260  
DB |||||  
QY 1201 ACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATATCTGCTTTTCTGGTACCTAC 1260  
DB |||||  
QY 1261 ATTCTCTCCCTCTTCTGCAAGGCTATCATTTTACAGCTGATTCTTGGGAGCAGCATCCAT 1320  
DB |||||  
QY 1261 ATTCTCTCCCTCTTCTGCAAGGCTATCATTTTACAGCTGATTCTTGGGAGCAGCATCCAT 1320  
DB |||||  
QY 1321 TTTTATTTGGCAAGATCCAGGGCAGCGCGCTGGACTTTGGGCTTACATGCTGAACTTG 1380  
DB |||||  
QY 1321 TTTTATTTGGCAAGATCCAGGGCAGCGCGCTGGACTTTGGGCTTACATGCTGAACTTG 1380  
DB |||||  
QY 1381 ACCAATGATCCAGCTGAGCAACATTTGTCCACACCTCTCTCCACCTCCACCTAA 1437  
DB |||||  
QY 1381 ACCAATGATCCAGCTGAGCAACATTTGTCCACACCTCTCTCCACCTCCACCTAA 1437  
DB |||||



Db 901 ACCCCCTGCACCAAGAGATTGTGAGATGACTCTTCCATCTTCAGCAGTTTGAAATCCAGGCT 960  
Qy 961 ATTGGAACCTATCAACATGCCATCAAGCATCCTGGAGCTCTTCAACACCAGTTACTGC 1020  
Db 961 ATTGGAACCTATCAACATGCCATCAAGCATCCTGGAGCTCTTCAACACCAGTTACTGC 1020  
Qy 1021 CCTTACTCCAGGTGCGCTTCAATGGATTTTCTTGCCACCACTCCAGGGGGATTTTGGG 1080  
Db 1021 CCTTACTCCAGGTGCGCTTCAATGGATTTTCTTGCCACCACTCCAGGGGGATTTTGGG 1080  
Qy 1081 GCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGAAAGTCTCT 1140  
Db 1081 GCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGAAAGTCTCT 1140  
Qy 1141 CAGGAAAAGTGATGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAA 1200  
Db 1141 CAGGAAAAGTGATGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAA 1200  
Qy 1201 ACATCTTACGCTGAGTAAAGGAGAGTACCTCAGTGAATACCTGTTTCTGTACTCTAC 1260  
Db 1201 ACATCTTACGCTGAGTAAAGGAGAGTACCTGAGTGAATACCTGTTTCTGTACTCTAC 1260  
Qy 1261 ATTCTCTCCCTCTCTGCAAGGCTATCAATTTACAGCTGATTTCTCCCACTCCACCTAA 1320  
Db 1261 ATTCTCTCCCTCTCTGCAAGGCTATCAATTTACAGCTGATTTCTCCCACTCCACCTAA 1320  
Qy 1321 TTCAATTTGGCAAGATCCAGGCGAGGAGCGCGCTGGACTTTGGGCTACATCTGGAACCTG 1380  
Db 1321 TTCAATTTGGCAAGATCCAGGCGAGGAGCGCGCTGGACTTTGGGCTACATCTGGAACCTG 1380  
Qy 1381 ACCAATGATATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCACCTAA 1437  
Db 1381 ACCAATGATATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCACCTAA 1437

RESULT 3  
AAD00209  
ID AAD00209 standard; DNA; 1464 BP.  
AC AAD00209;  
XX XX  
DT 17-AUG-2000 (first entry)  
XX XX  
DE Human soluble CD39 fusion DNA construct, pIL2LFlagSolCD39.  
XX XX  
KW Soluble CD39; human; apyrase activity; platelet activation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;  
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;  
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;  
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;  
KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.  
XX XX  
OS Homo sapiens.  
OS Synthetic.

Key Location/Qualifiers  
FT 1..1464  
FT CDS  
FT /\*tag= a  
FT /product= "Fusion protein of pIL2LFlagSolCD39"  
FT sig\_peptide 1..72  
FT /\*tag= b  
FT /note= "Human interleukin 2 (hIL2) leader sequence"  
FT mat\_peptide 73..108  
FT /\*tag= c  
FT /product= "Mature human interleukin 2 N-terminal end"  
FT misc\_feature 109..120  
FT /\*tag= d  
FT /note= "Linker sequence"  
FT misc\_feature 121..144  
FT /\*tag= e  
FT /note= "FLAG tag sequence"

misc\_feature 145..1461  
/\*tag= e  
/note= "Coding region of human soluble CD39 (solCD39)"  
XX  
PN WO200023459-A1.  
XX  
PD 27-APR-2000.  
XX  
PF 13-OCT-1999; 99WO-US022955.  
XX  
PR 16-OCT-1998; 98US-0104585P.  
PR 06-NOV-1998; 98US-0107466P.  
PR 13-AUG-1999; 99US-0149010P.  
XX (IMMV ) IMMUNEX CORP.  
PA Maliszewski CR, Gayle RB, Price VL, Gimpel SD;  
XX PI  
XX P-PSDB; AAV70921.  
DR WPI; 2000-339644/29.  
XX  
XX New soluble CD39 polypeptides having apyrase activity, useful for  
PT inhibiting angiogenesis and treating unstable angina, myocardial  
PT infarction, stroke, coronary artery disease or injury.  
XX  
PS Example 9; Page 107-109; 122pp; English.  
XX  
CC The present DNA sequence is a fusion construct pIL2LFlagSolCD39,  
CC comprising the leader peptide of human interleukin 2 (hIL2), 12 amino  
CC acids from the mature N-terminus of hIL2, a linker, FLAG tag sequence and  
CC soluble CD39 (solCD39) coding region, that has apyrase activity. This  
CC produces high levels of solCD39 expression and activity in the  
CC transfected cells. Soluble CD39 is constructed by removing the N- and C-  
CC terminal transmembrane domains. It retains the capacity to metabolise ATP  
CC and ADP at relevant concentrations and the ability to block and reverse  
CC ADP-induced platelet activation and recruitment, including platelet  
CC aggregation. Soluble CD39 polypeptides are useful for inhibiting  
CC angiogenesis. It is useful for the treatment of unstable angina,  
CC myocardial infarction, stroke, coronary artery disease or injury,  
CC atherosclerosis, peripheral vascular occlusion, pre-eclampsia, embolism,  
CC platelet-associated ischaemic disorders including lung, coronary and  
CC cerebral ischaemia, thrombotic disorders including coronary, peripheral  
CC and cerebral artery thrombosis, intracardiac and venous thrombosis,  
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and  
CC transient ischaemic attack. Soluble CD39 is also useful for preventing  
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or  
CC restenosis of blood vessels or stroke  
XX  
SQ Sequence 1464 BP; 424 A; 340 C; 342 G; 358 T; 0 U; 0 Other;  
Query Match 97.4%; Score 1400; DB 3; Length 1464;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1437; Conservative 0; Mismatches 0; Indels 27; Gaps 1;  
Qy 1 ATGGCCCTGTGGATCGACAGGATGCAACTCTCTTGTGATTGCACTAAGTCTTGCACCT 60  
Db 1 ATGGCCCTGTGGATCGACAGGATGCAACTCTCTTGTGATTGCACTAAGTCTTGCACCT 60  
Qy 61 GTCACAAAACAGTGCACCTACTCTCAAGATTCTCAAGAAAAACAGCTAAGTTC--- 116  
Db 61 GTCACAAAACAGTGCACCTACTCTCAAGTTCTACAAAGAAAAACAGCTAAGTTCAGGA 120  
Qy 117 -----AACCCAGAACAGCATTGCCAGAAAACGTTAAGTAT 153  
Db 121 GACTACAAAGATGACGATGACAAAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTAT 180  
Qy 154 GGGATTGTCTGGATGCGGGTTCTTCTCACAAAGTTTATACATCTATTAAGTGCCAGCA 213  
Db 181 GGGATTGTCTGGATGCGGGTTCTTCTCACAAAGTTTATACATCTATTAAGTGCCAGCA 240  
Qy 214 GAAAAGGAGAGATGACACAGCGGTGGTGCATCAAGTAGAAGATGACAGGGTTAAAGTCTCT 273  
Db 241 GAAAAGGAGAGATGACACAGCGGTGGTGCATCAAGTAGAAGATGACAGGGTTAAAGTCTCT 300

QY 274 GGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGCAATTTTACTGTACTGATTCATG 333  
DB |||||  
QY 301 GGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGCAATTTTACTGTACTGATTCATG 360  
DB |||||  
QY 334 GAAAGAGCTAGGGAAGTATCCAAAGTCCAGCACCAGCAAGAGACACCCGTTTACCTGGGA 393  
DB |||||  
QY 361 GAAAGAGCTAGGGAAGTATCCAAAGTCCAGCACCAGCAAGAGACACCCGTTTACCTGGGA 420  
DB |||||  
QY 394 GCCACGGCAGGATCGGTTGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTG 453  
DB |||||  
QY 421 GCCACGGCAGGATCGGTTGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTG 480  
DB |||||  
QY 454 GATGTGGTGGAGGAGCCTCAGCAACTACCCCTTTTGACTTCCAGGGTCCAGGATCAATT 513  
DB |||||  
QY 481 GATGTGGTGGAGGAGCCTCAGCAACTACCCCTTTTGACTTCCAGGGTCCAGGATCAATT 540  
DB |||||  
QY 514 ACTGGCCAGAGGAGGTCCTATGCTGATTAATCTATCAATCTATCTGCTGGCAATTC 573  
DB |||||  
QY 541 ACTGGCCAGAGGAGGTCCTATGCTGATTAATCTATCAATCTATCTGCTGGCAATTC 600  
DB |||||  
QY 574 AGTCAGAAAACAAAGTGGTTTCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTT 633  
DB |||||  
QY 601 AGTCAGAAAACAAAGTGGTTTCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTT 660  
DB |||||  
QY 634 GGAGCTTTGGACCTTGGGGGAGCCTCTACACAAAGTCACTTTTGTATCCCAAAACAGACT 693  
DB |||||  
QY 661 GGAGCTTTGGACCTTGGGGGAGCCTCTACACAAAGTCACTTTTGTATCCCAAAACAGACT 720  
DB |||||  
QY 694 ATCGAGTCCCAAGATAATGCTCTGCATTTTCCCTCTATGGCAAGGACTACATGCTCTAC 753  
DB |||||  
QY 721 ATCGAGTCCCAAGATAATGCTCTGCATTTTCCCTCTATGGCAAGGACTACATGCTCTAC 780  
DB |||||  
QY 754 ACACATAGCTCTTGTGCTATGGGAGGATCAGGCACCTCTGCAGAAACTGGCCCAAGGAC 813  
DB |||||  
QY 781 ACACATAGCTCTTGTGCTATGGGAGGATCAGGCACCTCTGCAGAAACTGGCCCAAGGAC 840  
DB |||||  
QY 814 ATTCAAGTTGCAAGTAATGAATTTCTCAGGAGCCCATGCTTTTCATCTCGATATAGAAG 873  
DB |||||  
QY 841 ATTCAAGTTGCAAGTAATGAATTTCTCAGGAGCCCATGCTTTTCATCTCGATATAGAAG 900  
DB |||||  
QY 874 TAGTGAAGTAAGTGACCTTTTACAGACCCCTCTGCACCAAGATTTGAGATGACTCTT 933  
DB |||||  
QY 901 TAGTGAAGTAAGTGACCTTTTACAGACCCCTCTGCACCAAGATTTGAGATGACTCTT 960  
DB |||||  
QY 934 CAAATCCAGCAGTTTGAATCCAGGATTTGAAACTATGAAACTATCAACAATGCCATCAAGCATC 993  
DB |||||  
QY 961 CAAATCCAGCAGTTTGAATCCAGGATTTGAAACTATGAAACTATCAACAATGCCATCAAGCATC 1020  
DB |||||  
QY 994 CTGAGCTCTTCAACACCAAGTTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTTC 1053  
DB |||||  
QY 1021 CTGAGCTCTTCAACACCAAGTTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTTC 1080  
DB |||||  
QY 1054 TTGCCACCACTCAGGGGATTTTGGGGATTTTTCAGCTTTTACTTTGATGAAGTTT 1113  
DB |||||  
QY 1081 TTGCCACCACTCAGGGGATTTTGGGGATTTTTCAGCTTTTACTTTGATGAAGTTT 1140  
DB |||||  
QY 1114 TTAACCTTGACATCAGAGAACTCTCAGGAAAGAGTGACTGAGATGATGAAGTTTC 1173  
DB |||||  
QY 1141 TTAACCTTGACATCAGAGAACTCTCAGGAAAGAGTGACTGAGATGATGAAGTTTC 1200  
DB |||||  
QY 1174 TGTGCTCAGCCTTGGGAGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTG 1233  
DB |||||  
QY 1201 TGTGCTCAGCCTTGGGAGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTG 1260  
DB |||||  
QY 1234 AGTGAATATGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTTC 1293  
DB |||||  
QY 1261 AGTGAATATGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTTC 1320  
DB |||||  
QY 1294 ACAGCTGATCTCTGGGAGACATCCATTTCTATGGCAAGATCCAGGGCAGCGCCGCG 1353  
DB |||||  
QY 1321 ACAGCTGATCTCTGGGAGACATCCATTTCTATGGCAAGATCCAGGGCAGCGCCGCG 1380  
DB |||||

QY 1354 TGGACTTTGGGTACATGCTGAACCTGACCAACATGATCCCAAGCTGAGCAACATTTGTC 1413  
DB |||||  
QY 1381 TGGACTTTGGGTACATGCTGAACCTGACCAACATGATCCCAAGCTGAGCAACATTTGTC 1440  
DB |||||  
QY 1414 ACACCTCTCTCCCACTCCACCTAA 1437  
DB |||||  
QY 1441 ACACCTCTCTCCCACTCCACCTAA 1464  
DB |||||  
RESULT 4  
AAD00204  
ID AAD00204 standard; DNA; 1464 BP.  
XX  
AC AAD00204;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Coding region of soluble CD39 expression plasmid.  
KW Soluble CD39; ADP-induced platelet activation; stroke; platelet aggregation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; anti-angiogenic; cardiant;  
KW cerebroprotective; anti-arteriosclerotic; vasodilator; anticoagulant;  
KW coronary ischaemia; vascular occlusion; solid CD39 expression plasmid; ss.  
XX Homo sapiens.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 1..1464  
FT /tag= b  
FT /product= "solCD39 expression plasmid protein"  
FT sig\_peptide  
FT 1..72  
FT /tag= a  
FT /note= "hulL2 leader sequence"  
FT mat\_peptide  
FT 73..108  
FT /tag= c  
FT /product= "Mature human IL2"  
FT /note= "First N-terminal 12 amino acids"  
FT misc\_feature  
FT 109..120  
FT /tag= d  
FT /label= linker  
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FT 121..144  
FT /tag= e  
FT /note= "Flag tag"  
FT mat\_peptide  
FT 145..1461  
FT /tag= f  
FT /product= "Sol CD39"  
XX WO200023094-A2.  
PN  
XX  
XX 27-APR-2000.  
XX  
XX 13-OCT-1999; 99WO-US023641.  
XX  
PR 16-OCT-1998; 98US-0104585P.  
PR 06-NOV-1998; 98US-0107466P.  
PR 13-AUG-1999; 99US-0149010P.  
XX  
PA (IMMV ) IMMUNEX CORP.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Maliszewski CR, Gayle RB, Marcus AJ;  
XX  
XX WPI; 2000-339518/29.  
DR P-FSDB; AAY70898.  
XX  
XX Inhibiting platelet activation and recruitment, useful for treating a

mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.

Example 9; Page 107-109; 118pp; English.

The present sequence is the coding region of soluble CD39(solCD39) expression plasmid. This was used for the transient expression of solCD39 protein in mammalian expression systems. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke

Sequence 1464 BP; 424 A; 340 C; 342 G; 358 T; 0 U; 0 Other;

Query Match 97.4%; Score 1400; DB 3; Length 1464;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1437; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

1 ATGGCCCTGGATCGACGATGCAACTCCTCTTGGATTGCACTNAGTCTTGACATT 60  
1 ATGGCCCTGGATCGACGATGCAACTCCTCTTGGATTGCACTNAGTCTTGACATT 60  
61 GTCAAAACAGTGCACCTACTTCAAGTTCTACAAAGAAACACAGCTAAGTCTTC 116  
61 GTCAAAACAGTGCACCTACTTCAAGTTCTACAAAGAAACACAGCTAAGTCTTC 120  
117 -----AACCAGAAACAAAGCATTCGCCAGAAACGTTAAGTAT 153  
121 GACTACAAAGATGACGATGCAAAACCCAGAACAAAGCATTCGCCAGAAACGTTAAGTAT 180  
154 GGGATTGCTGGATCGGGTCTTCTCACAAGTTTATACATCTATAGTGGCCAGCA 213  
181 GGGATTGCTGGATCGGGTCTTCTCACAAGTTTATACATCTATAGTGGCCAGCA 240  
214 GAAAGAGAGATGACACAGCGTGGTGCATCAAGTAGAAGATGCGAGGGTTAAAGTCT 273  
241 GAAAGAGAGATGACACAGCGTGGTGCATCAAGTAGAAGATGCGAGGGTTAAAGTCT 300  
274 GGAATCTCAAAATTTGTTAGAAAGTAAATGAAATAGGCATTTACCTGATGATG 333  
301 GGAATCTCAAAATTTGTTAGAAAGTAAATGAAATAGGCATTTACCTGATGATG 360  
334 GAAAGAGTGGGAGGATTCAGAGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 393  
361 GAAAGAGTGGGAGGATTCAGAGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420  
394 GCACGCGAGCATGCGGTTGCTCAGGATGCAAGTGAAGTGGCAGACAGGGTTCTG 453  
421 GCACGCGAGCATGCGGTTGCTCAGGATGCAAGTGAAGTGGCAGACAGGGTTCTG 480  
454 GATGTGGTGGAGGAGGAGCCTCAGCAATACCCCTTTGACTTCAGGGTGCAGGATCAT 513  
481 GATGTGGTGGAGGAGGAGCCTCAGCAATACCCCTTTGACTTCAGGGTGCAGGATCAT 540  
514 ACTGGCCAGAGGAGGAGTGGCTGATGATGATGATGATGATGATGATGATGATGAT 573  
541 ACTGGCCAGAGGAGGAGTGGCTGATGATGATGATGATGATGATGATGATGATGAT 600  
574 AGTCAGAAAAACAGGTGGTTGAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTT 633  
601 AGTCAGAAAAACAGGTGGTTGAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTT 660  
634 GGAGCTTTGGACCTTGGGGAGGCTCTACAAAGTCACTTTTGTACCCCAAAACAGAGCT 693  
661 GGAGCTTTGGACCTTGGGGAGGCTCTACAAAGTCACTTTTGTACCCCAAAACAGAGCT 720

694 ATCGAGTCCCAGATAATGCTCTGCAATTTCCCTCTATGGCAAGGACTACAAATGCTTAC 753  
721 ATCGAGTCCCAGATAATGCTCTGCAATTTCCCTCTATGGCAAGGACTACAAATGCTTAC 780  
754 ACACATAGCTTCTTGCTATATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCCAAGGAC 813  
781 ACACATAGCTTCTTGCTATATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCCAAGGAC 840  
814 ATTCAGGTGCAAGTAATGAAATTTCTCAGGACCCCTGACCAAGAGATTTGAGATGACTCTT 933  
841 ATTCAGGTGCAAGTAATGAAATTTCTCAGGACCCCTGACCAAGAGATTTGAGATGACTCTT 960  
874 GTAGTGAACGTAAGTGACCTTTTACAAAGACCCCTGACCAAGAGATTTGAGATGACTCTT 993  
901 GTAGTGAACGTAAGTGACCTTTTACAAAGACCCCTGACCAAGAGATTTGAGATGACTCTT 960  
934 CCATTTCCAGCAGTGTGAAATCCAGGGTATTTGAAACTATCAACAATGCGATCAAAAGCATC 993  
961 CCATTTCCAGCAGTGTGAAATCCAGGGTATTTGAAACTATCAACAATGCGATCAAAAGCATC 1020  
994 CTGGAGCTCTTCAACACCAAGTTACTGCCCCCTTACTCCAGTGTGCTTCAATGGGATTTTC 1053  
1021 CTGGAGCTCTTCAACACCAAGTTACTGCCCCCTTACTCCAGTGTGCTTCAATGGGATTTTC 1080  
1054 TTGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCTTTTCTGTTGATGAAGTTT 1113  
1081 TTGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCTTTTCTGTTGATGAAGTTT 1140  
1114 TTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGATGATGATGAT 1173  
1141 TTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGATGATGATGAT 1200  
1174 TGTGCTCAGCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTG 1233  
1201 TGTGCTCAGCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTG 1260  
1234 AGTGAATACCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCT 1293  
1261 AGTGAATACCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCT 1320  
1294 ACAGCTGATTCCTGGAGCAGATCATTTCATTTGCAAGATCCAGGGCAGCAGCGCGC 1353  
1321 ACAGCTGATTCCTGGAGCAGATCATTTCATTTGCAAGATCCAGGGCAGCAGCGCGC 1380  
1354 TGGACTTTGGGCTACATGCTGAACTGACCAACATGATCCCAACATGATCCCAACATGATCC 1413  
1381 TGGACTTTGGGCTACATGCTGAACTGACCAACATGATCCCAACATGATCCCAACATGATCC 1440  
1414 ACACCTCTCTCCCACTCCACCTAA 1437  
1441 ACACCTCTCTCCCACTCCACCTAA 1464

RESULT 5

AAD00206

ID AAD00206 standard; DNA; 1365 BP.

XX AAD00206;

DT 17-AUG-2000 (first entry)

XX Human soluble CD39 and IL2 N-terminus comprising fusion DNA construct.

XX Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.

OS Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
XX CDS 1. .1365  
XX /tag= a  
XX /product= "Fusion protein of human Interleukin 2 (IL2) N-terminus and human soluble CD39 protein"  
XX misc\_feature 1. .45  
XX /tag= b  
XX /notes= "N-terminus of mature human interleukin 2 (IL2) "  
XX misc\_feature 45..1362  
XX /tag= c  
XX /notes= "Coding region of human soluble CD39 (solCD39) "  
XX WO200023459-A1.  
XX 27-APR-2000.  
XX 13-OCT-1999; 99WO-US022955.  
XX 16-OCT-1998; 98US-0104585P.  
XX 06-NOV-1998; 98US-0107466P.  
XX 13-AUG-1999; 99US-0149010P.  
XX (IMMV ) IMMUNEX CORP.  
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;  
XX WPI: 2000-339644/29.  
XX P-PSDB; AAY0913.  
XX New soluble CD39 polypeptides having apyrase activity, useful for  
XX inhibiting angiogenesis and treating unstable angina, myocardial  
XX infarction, stroke, coronary artery disease or injury.  
XX Claim 11a; Page 93-95; 122pp; English.  
XX The present DNA sequence is a fusion construct, comprising the N-terminal  
XX region of mature human interleukin2 (IL2) and soluble CD39 (solCD39)  
XX coding region, having apyrase activity. This results in high levels of  
XX solCD39 expression and activity in the transfected cells. Soluble CD39 is  
XX constructed by removing the N- and C-terminal transmembrane domains. It  
XX retains the capacity to metabolise ATP and ADP at relevant concentrations  
XX and the ability to block and reverse ADP-induced platelet activation and  
XX recruitment, including platelet aggregation. Soluble CD39 polypeptides  
XX are useful for inhibiting angiogenesis. It is useful for the treatment of  
XX unstable angina, myocardial infarction, stroke, coronary artery disease  
XX or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia,  
XX embolism, platelet-associated ischaemic disorders including lung,  
XX coronary and cerebral ischaemia, thrombotic disorders including coronary,  
XX peripheral and cerebral artery thrombosis, intracardiac and venous  
XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
XX for preventing thrombus formation or reformation, occlusion, reocclusion,  
XX stenosis or restenosis of blood vessels or stroke  
SQ Sequence 1365 BP; 394 A; 317 C; 319 G; 335 T; 0 U; 0 Other;  
Query Match 95.0%; Score 1365; DB 3; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 73 GCACCTACTCAAGTTCTACAAAGAAACACAGCTAACTAGTTCAACCCAGACAAAGCA 132  
Db 1 GCACCTACTCAAGTTCTACAAAGAAACACAGCTAACTAGTTCAACCCAGACAAAGCA 60  
QY 133 TTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGGGGTTCTTCTCACACAAGTTTA 192  
Db 61 TTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGGGGTTCTTCTCACACAAGTTTA 120  
QY 193 TACATCTATAGTGGCCAGCAAGAAAGAGAAATGACACAGGCGTGGTGCATCAAGTAGAA 252  
|||||

Db 121 TACATCTATAGTGGCCAGCAAGAAAGAGAAATGACACAGGCGTGGTGCATCAAGTAGAA 180  
QY 253 GAATGCAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTTTCAGAAAGTAAATGAAATAGGC 312  
Db 181 GAATGCAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTTTCAGAAAGTAAATGAAATAGGC 240  
QY 313 ATTTACCTGACTGATTTGATGGAAGAGAGCTAGGGAAGTGTATTCGAAGGTCACAGACCAA 372  
Db 241 ATTTACCTGACTGATTTGATGGAAGAGAGCTAGGGAAGTGTATTCGAAGGTCACAGACCAA 300  
QY 373 GAGACACCCGTTTACCTGGGAGCCACGCGCATCGCGTTCCTCAGATGGAAAGTGA 432  
Db 301 GAGACACCCGTTTACCTGGGAGCCACGCGCATCGCGTTCCTCAGATGGAAAGTGA 360  
QY 433 GAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGGAGCCTCAGCAACTACCCCTTTGAC 492  
Db 361 GAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGGAGCCTCAGCAACTACCCCTTTGAC 420  
QY 493 TTCCAGGGTGCAGGATCATTTACTGGCCAAAGAGAGGAGTGTCTATGGCTGGATTAATATC 552  
Db 421 TTCCAGGGTGCAGGATCATTTACTGGCCAAAGAGAGGAGTGTCTATGGCTGGATTAATATC 480  
QY 553 AACTATCTGCTGGCGCAATTCAGTCAGAAACAAAGTGTGTTCAGCATAGTCCCATATGA 612  
Db 481 AACTATCTGCTGGCGCAATTCAGTCAGAAACAAAGTGTGTTCAGCATAGTCCCATATGA 540  
QY 613 ACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGGCTCTACACAAGTCACT 672  
Db 541 ACCAATAATCAGGAAACCTTTGGAGCTTTGGAGCTTTGGGGAGGCTCTACACAAGTCACT 600  
QY 673 TTTGTACCCCAAAACCAGACTATCGAGTCCCAAGATATGCTGTGCAATTTGGCTCTAT 732  
Db 601 TTTGTACCCCAAAACCAGACTATCGAGTCCCAAGATATGCTGTGCAATTTGGCTCTAT 660  
QY 733 GGCAAGGACTACAATGTCTACACATAGCTTCTGTGCTATGGGAAGATCAGGACTC 792  
Db 661 GGCAAGGACTACAATGTCTACACATAGCTTCTGTGCTATGGGAAGATCAGGACTC 720  
QY 793 TGGCAGAAACCTGGCCAGGACATTCAGGTTCCAAAGTAAATGAAATTTCTCAGGAGACCATGC 852  
Db 721 TGGCAGAAACCTGGCCAGGACATTCAGGTTCCAAAGTAAATGAAATTTCTCAGGAGACCATGC 780  
QY 853 TTTTCATCTGGATATAAGAGGTTAGTGAACCTAAGTGAACCTTTACAGACCCCTGCACC 912  
Db 781 TTTTCATCTGGATATAAGAGGTTAGTGAACCTAAGTGAACCTTTACAGACCCCTGCACC 840  
QY 913 AAGAGATTTGAGATGACTTCCATTCAGCAGATTTGAAATCCAGGTTATTTGGAACCTAT 972  
Db 841 AAGAGATTTGAGATGACTTCCATTCAGCAGATTTGAAATCCAGGTTATTTGGAACCTAT 900  
QY 973 CAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACACAGTACTGCGCTTACTCCAG 1032  
Db 901 CAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACACAGTACTGCGCTTACTCCAG 960  
QY 1033 TGTGCTTCAATGGATTTTCTTCCCACTCAGGCGGATTTTGGGGGCAATTTTCAGCT 1092  
Db 961 TGTGCTTCAATGGATTTTCTTCCCACTCAGGCGGATTTTGGGGGCAATTTTCAGCT 1020  
QY 1093 TTTTACTTTGTGATGAAGTTTAACTTGACATCAGAAAGTCTCTCAGAAAAAGTG 1152  
Db 1021 TTTTACTTTGTGATGAAGTTTAACTTGACATCAGAAAGTCTCTCAGAAAAAGTG 1080  
QY 1153 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGGAGATAAAAACATCTTACGCT 1212  
Db 1081 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGGAGATAAAAACATCTTACGCT 1140  
QY 1213 GGAGTAAAGGAGAGTACCTGAGTGAATACCTGCTTTTTCTGGTACCTACATTTCTCTCCCTC 1272  
Db 1141 GGAGTAAAGGAGAGTACCTGAGTGAATACCTGCTTTTTCTGGTACCTACATTTCTCTCCCTC 1200  
QY 1273 CTTCTGCAAGGCTATCATTTTCAGAGCTGATTCCTGGAGACATCCATTTTCATTTGGCAAG 1332  
Db 1201 CTTCTGCAAGGCTATCATTTTCAGAGCTGATTCCTGGGAGACATCCATTTTCATTTGGCAAG 1260



QY 1333 ATCCAGGCGAGCAGCCGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1392  
|||||  
Db 1261 ATCCAGGCGAGCAGCCGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320  
|||||  
QY 1393 CCAGCTGAGCAACCAATTTGTCACACACTCTCTCCCACTCCACCTAA 1437  
|||||  
Db 1321 CCAGCTGAGCAACCAATTTGTCACACACTCTCTCCCACTCCACCTAA 1365  
|||||

RESULT 6  
AAD00201  
ID AAD00201 standard; cDNA; 1365 BP.

AC AAD00201;

XX 17-AUG-2000 (first entry)

DE Fusion construct of human soluble CD39 cDNA-1.

XX Soluble CD39; ADP-induced platelet activation; platelet aggregation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;  
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH 1. .1365  
CDS

FT /\*tag= a  
FT /product= "Human soluble CD39 protein"

XX W0200023094-A2.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US023641.

XX 16-OCT-1998; 98US-0104585P.

PR 06-NOV-1998; 98US-0107466P.

PR 13-AUG-1999; 99US-0149010P.

XX (IMV ) IMMUNEX CORP.  
PA (CORR ) CORNELL RES FOUND INC.

XX Maliszewski CR, Gayle RB, Marcus AJ;

XX WPI; 2000-339518/29.

DR P-PSDB; AAY70890.

XX Inhibiting platelet activation and recruitment, useful for treating a

XX mammal suffering from unstable angina, myocardial infarction, stroke,

XX coronary artery disease or injury, comprises administering soluble CD39

XX polypeptides.

PS Claim 10; Page 93-95; 11pp; English.

XX The present cDNA sequence is a fusion construct encoding sol(soluble)CD39  
CC having apyrase activity. Fusion of 12 amino acids from the N-terminus of  
CC mature human II2 to the solCD39 coding region results in high levels of  
CC both expression and activity in the supernatants of transfected cells.  
CC This is used in the treatment of unstable angina, myocardial infarction,  
CC stroke, coronary artery disease or injury, atherosclerosis, peripheral  
CC vascular occlusion, preclampsia, embolism, platelet-associated ischaemic  
CC disorder including lung ischaemia, coronary ischaemia and cerebral  
CC ischaemia, a thrombotic disorder including coronary artery thrombosis,

CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery  
CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous  
CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.  
CC Soluble CD39 is also useful for preventing thrombus formation or  
CC reformation, occlusion, reocclusion, stenosis or restenosis of blood  
CC vessels or stroke  
XX  
SQ Sequence 1365 BP; 394 A; 317 C; 319 G; 335 T; 0 U; 0 Other;

Query Match 95.0%; Score 1365; DB 3; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 GCACCTACTTCAAGTTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGAACCAAGCA 132

Db 1 GCACCTACTTCAAGTTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGAACCAAGCA 60

QY 133 TTGCCAGAAAACGTTAAGTATGGGATTGTGTGGATGCGGGTTCTTCTCACACAAGTTTA 192

Db 61 TTGCCAGAAAACGTTAAGTATGGGATTGTGTGGATGCGGGTTCTTCTCACACAAGTTTA 120

QY 193 TACATCTATAAGTGGCCAGCAGAAAAGGAGATGACACAGGCGTGGTGCATCAAGTAGAA 252

Db 121 TACATCTATAAGTGGCCAGCAGAAAAGGAGATGACACAGGCGTGGTGCATCAAGTAGAA 180

QY 253 GAATGCAGGGTTAAAGGCTCTGGAATCTCAAAATTTGTTTCAGAAAAGTAAATGAAATAGGC 312

Db 181 GAATGCAGGGTTAAAGGCTCTGGAATCTCAAAATTTGTTTCAGAAAAGTAAATGAAATAGGC 240

QY 313 ATTTACCTGACTGATTGATGGAAGAGCTAGGGAAGTATTCCAAGTCCAGACACCAA 372

Db 241 ATTTACCTGACTGATTGATGGAAGAGCTAGGGAAGTATTCCAAGTCCAGACACCAA 300

QY 373 GAGACACCCGTTTACTCGGGAGCCAGGCGAGCATGCGGTTGCTCAGGATGAAAAGTGA 432

Db 301 GAGACACCCGTTTACTCGGGAGCCAGGCGAGCATGCGGTTGCTCAGGATGAAAAGTGA 360

QY 433 GAGTTGGCAGACAGGGTTCTGGATGCTGGTGGAGAGAGGAGCCTCAGCAACTACCCCTTTGAC 492

Db 361 GAGTTGGCAGACAGGGTTCTGGATGCTGGTGGAGAGAGGAGCCTCAGCAACTACCCCTTTGAC 420

QY 493 TTCCAGGGTGCAGGATCATTTACTGCGCAAGAGAGGTGCTATGGCTGGATTACTATC 552

Db 421 TTCCAGGGTGCAGGATCATTTACTGCGCAAGAGAGGTGCTATGGCTGGATTACTATC 480

QY 553 AACTATCTGCTGGGCAAAATTAGTCAGAAAACAAGGTGGTTCCAGCATAGTCCCATATGA 612

Db 481 AACTATCTGCTGGGCAAAATTAGTCAGAAAACAAGGTGGTTCCAGCATAGTCCCATATGA 540

QY 613 ACCAATTAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACT 672

Db 541 ACCAATTAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACT 600

QY 673 TTTGTACCCCAAAACCCAGACTATCGAGTCCCAGATAAATGCTCGCAATTCGCTCTAT 732

Db 601 TTTGTACCCCAAAACCCAGACTATCGAGTCCCAGATAAATGCTCGCAATTCGCTCTAT 660

QY 733 GCGAGGACTCAATGCTTACACATAGCTTTCTGTGCTATGGGAGAGATCAGGCACCTC 792

Db 661 GCGAGGACTCAATGCTTACACATAGCTTTCTGTGCTATGGGAGAGATCAGGCACCTC 720

QY 793 TGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAAATTCCTCAGGACCCCATGC 852

Db 721 TGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAAATTCCTCAGGACCCCATGC 780

QY 853 TTTTCATCTCTGGATATAAGAAAGGTAGTGAAACGTAAGTGCATTTTACAAGACCCCTTCAC 912

Db 781 TTTTCATCTCTGGATATAAGAAAGGTAGTGAAACGTAAGTGCATTTTACAAGACCCCTTCAC 840

QY 913 AAGAGATTGAGATGACTCTTCCATCCAGCAGTTTGAATCCAGGGTATTGGAACTAT 972

Db 841 AAGAGATTGAGATGACTCTTCCATCCAGCAGTTTGAATCCAGGGTATTGGAACTAT 900



QY 973 CAACATGCCATCAAGCATCTGGAGCTCTTCAACACAGTTACTGCCCTTACTCCAG 1032  
Db 901 CAACATGCCATCAAGCATCTGGAGCTCTTCAACACAGTTACTGCCCTTACTCCAG 960  
QY 1033 TGTGCCCTTCAATGGGATTTCTTGCCACCACTCCAGGGGATTTGGGGCATTTTCAGCT 1092  
Db 961 TGTGCCCTTCAATGGGATTTCTTGCCACCACTCCAGGGGATTTGGGGCATTTTCAGCT 1020  
QY 1093 TTTTACTTTGTGATGAAGTTTAACTTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTG 1152  
Db 1021 TTTTACTTTGTGATGAAGTTTAACTTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTG 1080  
QY 1153 ACTGAGATGATGAAAAGTTCTGTGCTCAGCTTGGAGGAGATGAAAACATCTTACGCT 1212  
Db 1081 ACTGAGATGATGAAAAGTTCTGTGCTCAGCTTGGAGGAGATGAAAACATCTTACGCT 1140  
QY 1213 GGAGTAAGGAGAGTACCTGAGTGAATACTGCTTTCTGCTACCTTACATCTCTCCCTC 1272  
Db 1141 GGAGTAAGGAGAGTACCTGAGTGAATACTGCTTTCTGCTACCTTACATCTCTCCCTC 1200  
QY 1273 CTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGACACATCCATTTTCATTTGGCAAG 1332  
Db 1201 CTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGACACATCCATTTTCATTTGGCAAG 1260  
QY 1333 ATCCAGGGCAGGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1392  
Db 1261 ATCCAGGGCAGGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320  
QY 1393 CCAGCTGAGCAACACCTTGTCACACCTCTCTCCACTCCACCTAA 1437  
Db 1321 CCAGCTGAGCAACACCTTGTCACACCTCTCTCCACTCCACCTAA 1365

RESULT 7

AAD00205  
ID AAD00205 standard; cDNA; 1599 BP.  
XX

AC AAD00205;

DT 17-AUG-2000 (first entry)

DE Human soluble CD39 protein encoding cDNA.

KW Soluble CD39; human; apyrase activity; platelet activation; inhibitor;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;  
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;  
KW antithrombotic; cerebroprotective; antiarteriosclerotic; anticoagulant;  
KW cardiant; vasotropic; thrombolytic; ss.

OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT CDS 67..1599  
FT /\*tag= a  
FT /product= "Human soluble CD39 protein"  
FT /note= "Cell surface molecule"

XX WO200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US022955.

XX 16-OCT-1998; 98US-0104585P.

PR 06-NOV-1998; 98US-0107466P.

XX 13-AUG-1999; 99US-0149010P.

XX (IMV ) IMMUNEX CORP.

XX Maliszewski CR, Gayle RB, Price VL, GimpeI SB;

XX

DR WPI; 2000-339644/29.

XX P-PSDB; AAY70910.

PT New soluble CD39 polypeptides having apyrase activity, useful for  
PT inhibiting angiogenesis and treating unstable angina, myocardial  
PT infarction, stroke, coronary artery disease or injury.

XX Example 9; Page 85-87; 122pp; English.

XX The present sequence is the cDNA encoding the human soluble CD39 protein,  
CC a cell surface molecule, having apyrase activity. It is derived from a  
CC human B cell line cDNA library, referred to as MP-1. Soluble CD39 is  
CC constructed by removing the N- and C-terminal transmembrane domains. It  
CC retains the capacity to metabolise ATP and ADP at relevant concentrations  
CC and the ability to block and reverse ADP-induced platelet activation and  
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides  
CC are useful for inhibiting angiogenesis. It is useful for the treatment of  
CC unstable angina, myocardial infarction, stroke, coronary artery disease  
CC or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,  
CC embolism, platelet-associated ischaemic disorders including lung,  
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,  
CC peripheral and cerebral artery thrombosis, intracardiac and venous  
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
CC stenosis or restenosis of blood vessels or stroke

SQ Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;

Query Match 91.8%; Score 1319.2; DB 3; Length 1599;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAACGTTTAACTATGGGATTTGCTGGATCGG 172

Db 173 GGTGACCCAGAACAAAGCATTTGCCAGAAACGTTTAACTATGGGATTTGCTGGATCGG 232

QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGATGACACAG 232

Db 233 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGATGACACAG 292

QY 233 GCGTGGTGATCAAGTAGAAGATTCAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTTC 292

Db 293 GCGTGGTGATCAAGTAGAAGATTCAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTTC 352

QY 293 AGAAGTAAATGAATAGGCAATTTACCTGACTGATGGCAAGAGCTAGGGAAGTGA 352

Db 353 AGAAGTAAATGAATAGGCAATTTACCTGACTGATGGCAAGAGCTAGGGAAGTGA 412

QY 353 TTCCAAGTCCAGCACCAGACACACCCGTTTACCTGGGAGCCACGGCATGCGGT 412

Db 413 TTCCAAGTCCAGCACCAGACACACCCGTTTACCTGGGAGCCACGGCATGCGGT 472

QY 413 TGCTCAGGATGGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGCC 472

Db 473 TGCTCAGGATGGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGCC 532

QY 473 TCAGCAACTACCCCTTTTGACTTCCAGGGTGCAGGATCATTTACTGGCCCAAGAGGAGTG 532

Db 533 TCAGCAACTACCCCTTTTGACTTCCAGGGTGCAGGATCATTTACTGGCCCAAGAGGAGTG 592

QY 533 CCTATGGCTGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 592

Db 593 CCTATGGCTGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 652

QY 593 TCAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTTTGGAGCTTTTGGACCTTGGGG 652

Db 653 TCAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTTTGGAGCTTTTGGACCTTGGGG 712

QY 653 GAGCCTCTACCAAGTCACCTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG 712

Db 713 GAGCCTCTACCAAGTCACCTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG 772

QY	713	CTCTGCAATTTCCCTCTATGSCAAGGACTACAAATGCTACACACATAGCTTCTTGCT	772
Db	773	CTCTGCAATTTCCCTCTATGSCAAGGACTACAAATGCTACACACATAGCTTCTTGCT	832
QY	773	ATGGGAAGGATCAGGCACTCTGCGAGAAACTGCGCCAGGACATTCAGGTTGCAAGTAATG	832
Db	833	ATGGGAAGGATCAGGCACTCTGCGAGAAACTGCGCCAGGACATTCAGGTTGCAAGTAATG	892
QY	833	AAATTTCTCAGGGAACCCATGCTTTCATCTGCGATATAGAAGGTAAGTGAACGTGAAC	892
Db	893	AAATTTCTCAGGGAACCCATGCTTTCATCTGCGATATAGAAGGTAAGTGAACGTGAAC	952
QY	893	TTTACAGACCCCTCCACCAAGAGATTTGAGATGACTCTTCCATTCACGACGTTTGAA	952
Db	953	TTTACAGACCCCTCCACCAAGAGATTTGAGATGACTCTTCCATTCACGACGTTTGAA	1012
QY	953	TCAGGGTATTTGGAACATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA	1012
Db	1013	TCAGGGTATTTGGAACATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA	1072
QY	1013	GTTACTGCCCTTACTCCAGTGTCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG	1072
Db	1073	GTTACTGCCCTTACTCCAGTGTCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG	1132
QY	1073	ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGTGATGAAGTTTAAACTTTGACATCAGAG	1132
Db	1133	ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGTGATGAAGTTTAAACTTTGACATCAGAG	1192
QY	1133	AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTTCTGTCTGACGCTTGGGAGG	1192
Db	1193	AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTTCTGTCTGACGCTTGGGAGG	1252
QY	1193	AGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTTCTG	1252
Db	1253	AGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTTCTG	1312
QY	1253	GTACCTACATCTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGGAGC	1312
Db	1313	GTACCTACATCTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGGAGC	1372
QY	1313	ACATCAATTTTCAATGGCAACATCCAGGGACGACGCGGCTGGACTTTGGGCTACATGC	1372
Db	1373	ACATCAATTTTCAATGGCAACATCCAGGGACGACGCGGCTGGACTTTGGGCTACATGC	1432
QY	1373	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA	1432
Db	1433	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA	1492
QY	1433	CCTA 1436	
Db	1493	CCTA 1496	

RESULT 8	
AAD00200	
ID	AAD00200 standard; cDNA; 1599 BP.
XX	
AC	AAD00200;
XX	
DT	17-AUG-2000 (first entry)
XX	
DE	Human soluble CD39 cDNA.
XX	
KW	Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW	unstable angina; myocardial infarction; stroke; coronary artery disease;
KW	atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW	platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW	cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW	cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW	peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW	PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW	occlusion; reocclusion; stenosis; restenosis; antianginal; cardiac;

QY	113	GTTCAACCCAGAACAAAGCATTCGCCAGAAAAGCTTAAGTATCGGATTTGCTGGATCGG	172
Db	173	GCTTGACCCAGAACAAAGCATTCGCCAGAAAAGCTTAAGTATCGGATTTGCTGGATCGG	232
QY	173	GTTCTTCTCACACAAGTTTATACATCTATACTGCGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTC	232
Db	233	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAAAAAGGAGAATGACACAG	292
QY	233	GGCTGGTGCATCAAGTAGAAGTAATCAGGGTTTAAAGGTCCTCGAATCTCAAAATTTGTTTC	292
Db	293	GGCTGGTGCATCAAGTAGAAGTAATCAGGGTTTAAAGGTCCTCGAATCTCAAAATTTGTTTC	352
QY	293	AGAAAGTAATAAATAAGGACATTTTCTGACCTGATTTGCAATGGAAGAGCTAGGGAAGTGA	352
Db	353	AGAAAGTAATAAATAAGGACATTTTCTGACCTGATTTGCAATGGAAGAGCTAGGGAAGTGA	412

Query Match	91.8%;	Score 1319.2;	DB 3;	Length 1599;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1321;	Conservative	0;	Mismatches	3; Indels 0; Gaps 0;

cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;  
coronary ischaemia; vascular occlusion; ss.  
Homo sapiens.  
Key Location/Qualifiers  
CDS 67..1599  
/\*tag= a  
/product= "Soluble CD39 protein"

WO200023094-A2.  
27-APR-2000.  
13-OCT-1999; 99WO-US023641.  
16-OCT-1998; 98US-0104585P.  
06-NOV-1998; 98US-0107466P.  
13-AUG-1999; 99US-0149010P.  
(IMMV ) IMMUNEX CORP.  
(CORR ) CORNELL RES FOUND INC.  
PI Maliszewski CR, Gayle RB, Marcus AJ;  
WPI: 2000-339518/29.  
P-PSDB; AAY70887.  
Inhibiting platelet activation and recruitment, useful for treating a  
mammal suffering from unstable angina, myocardial infarction, stroke,  
coronary artery disease or injury, comprises administering soluble CD39  
polypeptides.

Example 10; Page 85-87; 118pp; English.  
The present cDNA sequence encodes soluble CD39 having apyrase activity.  
This was derived from a cDNA library prepared from a human B cell line  
referred to as MP-1. Soluble CD39 retains the capacity of wildtype CD39  
to metabolise ATP and ADP at physiologically relevant concentrations as  
well as the ability to block and reverse ADP-induced platelet activation  
and recruitment including platelet aggregation. This is used in the  
treatment of unstable angina, myocardial infarction, stroke, coronary  
artery disease or injury, atherosclerosis, peripheral vascular disorder including  
preclampsia, embolism, platelet-associated ischaemic disorder including  
lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic  
disorder including coronary artery thrombosis, cerebral artery  
thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous  
thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),  
pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also  
useful for preventing thrombus formation or reformation, occlusion,  
reocclusion, stenosis or restenosis of blood vessels or stroke

Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;

353 TTCCAAGTCCAGACCCAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATGCGGT 412  
413 TTCCAAGTCCAGACCCAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATGCGGT 472  
413 TGCTCAGGATGGAAGTGAAGTGGCAGACAGGGTCTGCTGATGTTGGTGGAGAGGCC 472  
473 TGCTCAGGATGGAAGTGAAGTGGCAGACAGGGTCTGCTGATGTTGGTGGAGAGGCC 532  
473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAAGGAAGGTG 532  
533 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAAGGAAGGTG 592  
533 CCTATGGCTGGATTAATACTATCAATCTCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTG 592  
593 CCTATGGCTGGATTAATACTATCAATCTCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTG 652  
593 TCAGCATAGTCCCATATGAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 652  
653 TCAGCATAGTCCCATATGAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 712  
653 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCGCAGATAATG 712  
713 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCGCAGATAATG 772  
713 CTCTCAATTTCCGCTCTATGCAAGGACTACAATGTCTTACACATAGCTTCTTTGTCT 772  
773 CTCTCAATTTCCGCTCTATGCAAGGACTACAATGTCTTACACATAGCTTCTTTGTCT 832  
773 ATGGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAGTTGCAAGTAATG 832  
833 ATGGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAGTTGCAAGTAATG 892  
833 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGTGTGAACGTAAGTGACC 892  
893 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGTGTGAACGTAAGTGACC 952  
893 TTACAAGACCCCTGCACCAAGAGATTTGAGATGACTTCTCCATTCAGCAGATTTGAAA 952  
953 TTACAAGACCCCTGCACCAAGAGATTTGAGATGACTTCTCCATTCAGCAGATTTGAAA 1012  
953 TCCAGGATATGGAACATATCAACATGCCATCAAGCATCTGAGCTCTTCAACACCA 1012  
1013 TCCAGGATATGGAACATATCAACATGCCATCAAGCATCTGAGCTCTTCAACACCA 1072  
1013 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTGACACCACTCCAGGGGG 1072  
1073 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTGACACCACTCCAGGGGG 1132  
1073 ATTTTGGGGCAATTTTCACTTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1132  
1133 ATTTTGGGGCAATTTTCACTTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1192  
1133 AAGTCTCTCAGAAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1192  
1193 AAGTCTCTCAGAAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1252  
1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATGCTTTTCTG 1252  
1253 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATGCTTTTCTG 1312  
1253 GTACCTACATCTCTCCCT 1312  
1313 GTACCTACATCTCTCCCT 1372  
1313 ACATCCATTTCAATGGCAAGTCCAGGGCAGGACCGCGGTGAGCTTTGGGCTACATGC 1372  
1373 ACATCCATTTCAATGGCAAGTCCAGGGCAGGACCGCGGTGAGCTTTGGGCTACATGC 1432  
1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATGTCACACCTCTCTCCCACTCCA 1432  
1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATGTCACACCTCTCTCCCACTCCA 1492

QY 1433 CCTA 1436  
Db 1493 CCTA 1496

RESULT 9  
ID ADL24294 standard; DNA; 1599 BP.  
XX ADL24294;  
AC ADL24294;  
XX 03-JUN-2004 (first entry)  
XX Human CD39 coding sequence.  
XX ds; Gene; cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30;  
XX OX40; antagonist.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT CDS 67..1599  
FT /\*tag= a  
FT /product= "CD39"  
XX  
XX WO2004019866-A2.  
XX PN 11-MAR-2004.  
XX PD 21-AUG-2003; 2003WO-US026354.  
XX PF 28-AUG-2002; 2002US-0406418P.  
XX PR 12-AUG-2003; 2003US-0494457P.  
XX PA (IMMV ) IMMUNEX CORP.  
XX PI Burton PB, Deisher TA;  
XX WPI; 2004-239107/22.  
XX P-PSDB; ADL24295.  
XX  
XX Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a  
XX cardiovascular disease, e.g. chronic immune myocarditis, congestive heart  
XX failure, aneurysm, angina, embolism, restenosis, ischemia or  
XX thrombocytopenic purpura.  
XX  
XX Disclosure; Page 130-132; 135pp; English.  
XX  
XX The present invention relates to a method of treating cardiovascular  
XX disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,  
XX CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40  
XX antagonists are useful for treating cardiovascular disorders, e.g.  
XX (chronic immune) myocarditis, congestive heart failure, aneurysms,  
XX angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The  
XX present sequence is a coding sequence used in the exemplification of the  
XX invention.  
XX  
XX Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;  
SQ

Query Match 91.8%; Score 1319.2; DB 12; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAACGTTTAAGTATGGATTGCTGGATCGG 172  
Db 173 GGTTCAGCCAGAACAAAGCATTTGCCAGAAACGTTTAAGTATGGATTGCTGGATCGG 232  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAAGAGAAATGACACAG 232  
Db 233 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAAGAGAAATGACACAG 292  
QY 233 GCGTGGTGCATCAAGTGAAGAAATGCGGGTTAAAGGTCCTTGAATCTCAAAATTTGTC 292

293 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 352  
293 AGAAGTAAATGAATAGGCAATTTACTGACTGATTTGTCATGGAAGAGCTTAGGGAATGA 352  
353 AGAAAGTAAATGAATAGGCAATTTACTGACTGATTTGTCATGGAAGAGCTTAGGGAATGA 412  
353 TTCCAAGGTCCTCAGCAGCAAGAGACACCCGCTTTACCTTGGGAGCCAGGCAAGGATCGGGT 412  
413 TTCCNAGGTCCTCAGCAGCAAGAGACACCCGCTTTACCTTGGGAGCCAGGCAAGGATCGGGT 472  
413 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGGCC 472  
473 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGGCC 532  
473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTACTGCGCAAGAGAGGTTG 532  
533 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTACTGCGCAAGAGAGGTTG 592  
533 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTTCAGAAAAACAAGTGGT 592  
593 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTTCAGAAAAACAAGTGGT 652  
593 TCAGCATAGTCCCCTATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 652  
653 TCAGCATAGTCCCCTATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 712  
653 GAGGCTCTACAAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCGAGATAATG 712  
713 GAGGCTCTACAAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCGAGATAATG 772  
713 CTCTGCAATTTGCGCTCTATGGAAGGACTACAAATGTTCTACACACATAGCTTCTGTGCT 772  
773 CTCTGCAATTTGCGCTCTATGGAAGGACTACAAATGTTCTACACACATAGCTTCTGTGCT 832  
773 ATGGGAAGTATCAGGCACTCTGGCAGAAATCGCCAAAGGACATTCAGGTTGCAAGTAATG 832  
833 ATGGGAAGTATCAGGCACTCTGGCAGAAATCGCCAAAGGACATTCAGGTTGCAAGTAATG 892  
833 AATTTCTCAGGAGCCCATGCTTTTCACTCTGGATATAGAAGGTAGTGAAGTAAAGTACC 892  
893 AATTTCTCAGGAGCCCATGCTTTTCACTCTGGATATAGAAGGTAGTGAAGTAAAGTACC 952  
893 TTTTACAGACCCCTGTCACCAAGAGATTTTCAGATGACTCTTCCATTTCCAGCAGTTTGAAA 952  
953 TTTTACAGACCCCTGTCACCAAGAGATTTTCAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1012  
953 TCCAGGGTATTTGGAAACTATCAACAATGCCATCAAGCATCTCTGGAGCTTCTCAACACCA 1012  
1013 TCCAGGGTATTTGGAAACTATCAACAATGCCATCAAGCATCTCTGGAGCTTCTCAACACCA 1072  
1013 GTTACTGCCCTTACTCCAGTGTGCTTTCAATGGGATTTTCTTGGCCACCATCTCAGGGGG 1072  
1073 GTTACTGCCCTTACTCCAGTGTGCTTTCAATGGGATTTTCTTGGCCACCATCTCAGGGGG 1132  
1073 ATTTTGGGGCATTTTACGCTTTTACTTTTGTGATGAAGTTTAAACTTGCACATCAGAGA 1132  
1133 ATTTTGGGGCATTTTACGCTTTTACTTTTGTGATGAAGTTTAAACTTGCACATCAGAGA 1192  
1133 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCCTTGGGAGG 1192  
1193 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCCTTGGGAGG 1252  
1193 AGATAAAACATCTTACGCTGGAGTAAAGAGAGTACCTTGAGTGAATACTGCTTTTCTG 1252  
1253 AGATAAAACATCTTACGCTGGAGTAAAGAGAGTACCTTGAGTGAATACTGCTTTTCTG 1312  
1253 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGC 1312  
1313 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGC 1372  
1313 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCAGCCGGCTGGACTTTGGGTACATGC 1372  
1373 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCAGCCGGCTGGACTTTGGGTACATGC 1432

QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCTCCCACTCCA 1432  
Db 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCTCCCACTCCA 1492  
QY 1433 CCTA 1436  
Db 1493 CCTA 1496  
RESULT 10  
AAA96069  
ID AAA96069 standard; DNA; 1704 BP.  
XX  
AC AAA96069;  
XX  
DT 29-JAN-2001 (first entry)  
XX Human ATP diphosphohydrolase coding sequence.  
DE  
XX Drug resistance; ATP gradient; chemotherapeutic; antibiotic; herbicide;  
KW human; ATP diphosphohydrolase; ds.  
KW Homo sapiens.  
XX  
OS  
XX  
PN WO200052144-A1.  
XX  
PD 08-SEP-2000.  
XX  
PF 28-FEB-2000; 2000WO-US0053315.  
XX  
PR 03-MAR-1999; 99US-00261825.  
XX  
PA (TEXA ) UNIV TEXAS.  
XX  
PI Thomas CE, Windsor JB, Roux SJ, Lloyd AM, Hurley L;  
XX WPI; 2000-587306/55.  
DR  
XX Increasing or decreasing drug resistance in target bacteria, yeast, plant  
PT or mammalian cells comprises altering ATP gradient across biological  
PT membrane of target cell.  
XX  
PS Claim 14; Page; 85pp; English.  
XX  
CC The present invention relates to a method for increasing or decreasing  
CC drug resistance in target bacteria, yeast, plant or mammalian cells by  
CC altering the ATP gradient across the biological membrane of the target  
CC cell. The method is useful for modulating drug resistance of cells. It is  
CC useful for increasing the sensitivity of cells to chemotherapeutic and  
CC antibiotic agents and increasing resistance to herbicides. The present  
CC sequence is human ATP diphosphohydrolase coding sequence. This sequence  
CC encodes was used in the present invention to modulate drug resistance.  
CC Note: The present sequence is not shown in the specification, but is  
CC referred to via its GenBank accession number  
XX  
SQ Sequence 1704 BP; 468 A; 392 C; 403 G; 441 T; 0 U; 0 Other;

Query Match 91.8%; Score 1319.2; DB 3; Length 1704;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCCG 172  
Db 137 GGTGACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCCG 196  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 232  
Db 197 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 256  
QY 233 GCGTGGTGCATCAAGTAGAAGAAATGAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 292  
Db 257 GCGTGGTGCATCAAGTAGAAGAAATGAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 316

QY 293 AGAAGTAAATAGGAATAGGATTTTAACTGACTGATTTGCAATGGAAAGAGCTAGGGAAGTGA 352  
DB 317 AGAAGTAAATAGGAATAGGATTTTACCTGACTGATTTGCAATGGAAAGAGCTAGGGAAGTGA 376  
QY 353 TTCCAAGGTTCCAGCACCAGACACCCGTTTACCTGGGAGCCACGGCAGGCGATCGGT 412  
DB 377 TTCCAAGGTTCCAGCACCAGACACCCGTTTACCTGGGAGCCACGGCAGGCGATCGGT 436  
QY 413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTCTTGGATGTGGTGGAGAGGCC 472  
DB 437 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTCTTGGATGTGGTGGAGAGGCC 496  
QY 473 TCAGCAACTACCCCTTTGATCTTCAGGGTCCAGGATCAATTAATGCGCCAGAGGAAGGTG 532  
DB 497 TCAGCAACTACCCCTTTGATCTTCAGGGTCCAGGATCAATTAATGCGCCAGAGGAAGGTG 556  
QY 533 CTTATGGCTGGATTAATCACTATCTCTGCTGGCAAAATTCAGTCAGAAACAAGGTGT 592  
DB 557 CTTATGGCTGGATTAATCACTATCTCTGCTGGCAAAATTCAGTCAGAAACAAGGTGT 616  
QY 593 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 652  
DB 617 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 676  
QY 653 GAGCCTCTACAAAGTCACTTTTGTATACCCCAAAACAGACTATCGAGTCCCAGATAATG 712  
DB 677 GAGCCTCTACAAAGTCACTTTTGTATACCCCAAAACAGACTATCGAGTCCCAGATAATG 736  
QY 713 CTTCTGCAATTTGGCCTCTATGCGCAAGGACTCAATGTCTACACATAGCTTCTTGCT 772  
DB 737 CTTCTGCAATTTGGCCTCTATGCGCAAGGACTCAATGTCTACACATAGCTTCTTGCT 796  
QY 773 ATGGGAAGGATCAGGCACTCTGCGAGAACTGCGCAAGGACATTCAGGTGCAAGTAATG 832  
DB 797 ATGGGAAGGATCAGGCACTCTGCGAGAACTGCGCAAGGACATTCAGGTGCAAGTAATG 856  
QY 833 AAATTTCTCAGGACCCATCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAGTGACC 892  
DB 857 AAATTTCTCAGGACCCATCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAGTGACC 916  
QY 893 TTACAGAGCCCTGACCAAGAGATTTGAGATGACTTTCATTCAGGATTCAGGATTTGAAA 952  
DB 917 TTACAGAGCCCTGACCAAGAGATTTGAGATGACTTTCATTCAGGATTCAGGATTTGAAA 976  
QY 953 TCCAGGTATTGAAACTATCAACATGCAATCAAGCACTCTGAGCTCTTCAACACCA 1012  
DB 977 TCCAGGTATTGAAACTATCAACATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1036  
QY 1013 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCACCCTCCAGGGGG 1072  
DB 1037 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCACCCTCCAGGGGG 1096  
QY 1073 ATTTTGGGGCATTTTTCAGCTTTTACTTTGATGAGTATTTTAACTTGATCAGAGA 1132  
DB 1097 ATTTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAACTTGATCAGAGA 1156  
QY 1133 AAGTCTCTCAGGAAAGGTGACTGAGATGATGATAAAGTTCTGCTCAGCCCTCGGAGG 1192  
DB 1157 AAGTCTCTCAGGAAAGGTGACTGAGATGATGATAAAGTTCTGCTCAGCCCTCGGAGG 1216  
QY 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACTGAGTGAATCTGCTTTTCTG 1252  
DB 1217 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACTGAGTGAATCTGCTTTTCTG 1276  
QY 1253 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTGGAGC 1312  
DB 1277 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTGGAGC 1336  
QY 1313 ACATCCATTTCAATTCGCAAGATCCAGGCGAGCGCGCTGGACTTTGGCTTACATGC 1372  
DB 1337 ACATCCATTTCAATTCGCAAGATCCAGGCGAGCGCGCTGGACTTTGGCTTACATGC 1396

QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCACTCCA 1432  
DB 1397 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCACTCCA 1456  
QY 1433 CCTA 1436  
DB 1457 CCTA 1460  
RESULT 11  
ADJ57261  
ID ADJ57261 standard; DNA; 1704 BP.  
XX  
AC ADJ57261;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human CD39 polypeptide encoding DNA.  
XX  
KW CD39; nucleoside diphosphate; thrombolytic; anticoagulant;  
KW cardiovascular; cytostatic; antibacterial; immunosuppressive; vasotropic;  
KW cardiant; antianginal; antiarteriosclerotic; gynaecological;  
KW cerebroprotective; cancer; human ; apyrase; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS 31..1563  
FT /\*tag= a  
FT /product= "CD39"  
XX  
PN WO2003070823-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 19-FEB-2003; 2003WO-US004845.  
XX  
PR 20-FEB-2002; 2002US-0358303P.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Elmaleh DR, Robson SC, Papisov MI;  
XX  
DR WPI; 2003-778966/73.  
XX  
P-PSDB; ADJ57262.  
XX  
PT New enzyme polymer conjugate used for treating abnormal levels of  
PT extracellular nucleotides or platelet aggregation, graft transplant,  
PT cardiovascular disease, cancer and sepsis.  
XX  
PS Disclosure; SEQ ID NO 1; 82pp; English.  
XX  
CC The invention relates to a conjugate (I) comprising an enzyme and a  
CC biodegradable polymer, where (i) enzymatic activity of the enzyme is  
CC higher relative to that of the enzyme in the absence of the biodegradable  
CC polymer, or (ii) the half life of the enzyme is longer than that of the  
CC enzyme in the absence of the polymer. The enzymatic activity (i) is at  
CC least 10 (preferably at least 100) times higher in the presence of the  
CC polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme,  
CC preferably an apyrase, especially a soluble form of CD39 and catalyzes  
CC hydrolysis of nucleoside diphosphate. The conjugate can be used to treat  
CC diseases relating to abnormal levels of extracellular nucleotides or  
CC abnormal aggregation of platelets, particularly cardiovascular disease,  
CC cancer, sepsis or a disease related to graft transplant. (I) is also used  
CC for treating coronary artery disease or injury following myocardial  
CC infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism,  
CC platelet associated ischaemic disorders including lung, coronary and  
CC cerebral ischaemia, reocclusion following thrombosis, thrombotic  
CC disorders, and thrombosis and coagulopathies associated with exposure to  
CC a foreign or injured tissue surface, in combination with angioplasty,  
CC carotid endarterectomy, anastomosis of vascular grafts and chronic  
CC cardiovascular devices. The present sequence represents a DNA encoding a





\_\_\_\_\_

PT aggregation - using CD39 protein with ATP di:phospho:hydrolase activity,

PT  
Gene

Gene therapy of inflammatory or immunological stimulation of platelet aggregation - using CD39 protein with ATP di-phospho-hydrolase activity.



PT useful for preventing or alleviating thrombotic condition in mammalian  
PT subject.  
XX

PS Claim 3; Page 38; 65pp; English.

XX Non-human transgenic or somatic recombinant mammals, whose cells contain  
CC a heterologous DNA encoding a polypeptide (especially human CD39 protein)  
CC having ATP-diphosphohydrolase activity under cellular activating  
CC conditions is claimed. In particular the animal is a pig and its cells  
CC (or tissues or organs) can be used for transplantation. DNA coding for  
CC human CD39 is also useful for genetically modifying a mammalian cell to  
CC render it less susceptible to an inflammatory or immunological stimulus  
CC and platelet aggregation. The modified cells can be used to prevent or  
CC alleviate a thrombotic condition. The present sequence encodes human CD39  
CC protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-3584  
XX

SQ Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

Query Match 91.8%; Score 1319.2; DB 2; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	113	GTTCAACCCCAAGCAATGCCAGAAACCGTTAAGTATGGGATGTGCTGGATGCGG	172
DB	174	GGTTGACCCAGAACAAAGCAATGCCAGAAACCGTTAAGTATGGGATGTGCTGGATGCGG	233
QY	173	GTTCTTCTCACACAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAAGGAGAATGACACAG	232
DB	234	GTTCTTCTCACACAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAAGGAGAATGACACAG	293
QY	233	GCCTGGTGCATCAAGTAGAAGAAATGAGGGTTAAAGTCTCGGAATCTCAAAATTTGTTTC	292
DB	294	GCCTGGTGCATCAAGTAGAAGAAATGAGGGTTAAAGTCTCGGAATCTCAAAATTTGTTTC	353
QY	293	AGAAAGTAAATGAAATAGGCAATTTACCTGATGATTCGATGGAAGAGAGCTAGGGAAGTGA	352
DB	354	AGAAAGTAAATGAAATAGGCAATTTACCTGATGATTCGATGGAAGAGAGCTAGGGAAGTGA	413
QY	353	TTCAAGGTTCCAGCACAAGACAACCCGGTTTACCTGGGAGCCAGGCGGATCGGCT	412
DB	414	TTCCAAAGGTTCCAGCACAAGACAACCCGGTTTACCTGGGAGCCAGGCGGATCGGCT	473
QY	413	TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGGAGCC	472
DB	474	TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGGAGCC	533
QY	473	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCCAAAGAGGAGTG	532
DB	534	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCCAAAGAGGAGTG	593
QY	533	CTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT	592
DB	594	CTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT	653
QY	593	TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGAGCTTTGGACCTTTGGGG	652
DB	654	TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGAGCTTTGGACCTTTGGGG	713
QY	653	GAGCCTCTACACAAGTCACATTTTGTATCCCAAAACACAGACTATCGAGTCCCCAGATAATG	712
DB	714	GAGCCTCTACACAAGTCACATTTTGTATCCCAAAACACAGACTATCGAGTCCCCAGATAATG	773
QY	713	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT	772
DB	774	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT	833
QY	773	ATGGGAGGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG	832
DB	834	ATGGGAGGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG	893
QY	833	AAATTTCTCAGGGACCCATGCTTTTCATCCTGGATATAGAAAGGTAGTGAACGTAAGTGACC	892
DB	894	AAATTTCTCAGGGACCCATGCTTTTCATCCTGGATATAGAAAGGTAGTGAACGTAAGTGACC	953

QY	893	TTTACAAGACCCCTGACCAAGAGATTGAGATGACTCTTCATTTCCAGCAGTTTGAAA	952
DB	954	TTTACAAGACCCCTGACCAAGAGATTGAGATGACTCTTCATTTCCAGCAGTTTGAAA	1013
QY	953	TCCAGGGTATTGGAAATATCAACAATGCCATCAAGACAATCTGGAGCTCTTTCAACACCA	1012
DB	1014	TCCAGGGTATTGGAAATATCAACAATGCCATCAAGACAATCTGGAGCTCTTTCAACACCA	1073
QY	1013	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCACACACTCCAGGGGG	1072
DB	1074	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCACACACTCCAGGGGG	1133
QY	1073	ATTTTGGGGCATTTTCAGCTTTTCTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA	1132
DB	1134	ATTTTGGGGCATTTTCAGCTTTTCTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA	1193
QY	1133	AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG	1192
DB	1194	AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG	1253
QY	1193	AGATAAAAACATCTTACGCTGGAGTAAAGGAAAGTACCTGAGTGAATACTGCTTTCTG	1252
DB	1254	AGATAAAAACATCTTACGCTGGAGTAAAGGAAAGTACCTGAGTGAATACTGCTTTCTG	1313
QY	1253	GTACCTTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAGCTGATTTCTGGGAGC	1312
DB	1314	GTACCTTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAGCTGATTTCTGGGAGC	1373
QY	1313	ACATCCATTTTCATTTGGCAAGATCCAGGGCAGGAGCGCGGCTGGACTTTGGGCTACATGC	1372
DB	1374	ACATCCATTTTCATTTGGCAAGATCCAGGGCAGGAGCGCGGCTGGACTTTGGGCTACATGC	1433
QY	1373	TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCATCCA	1432
DB	1434	TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCATCCA	1493
QY	1433	CCCTA 1436	
DB	1494	CCTA 1497	
RESULT 14			
ID	ADI32149	standard; cDNA; 1818 BP.	
XX	AC	ADI32149;	
XX	DT	17-JUN-2004 (first entry)	
XX	DE	Human cDNA #1475.	
XX	KW	Human; gene; ss; immunological response; immunopathological condition;	
XX	KW	Crohn's disease; asthma; ulcerative colitis; hyperesinophilia;	
XX	KW	irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;	
XX	KW	acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;	
XX	KW	osteopathic; antiarthritic; antirheumatic; cytostatic.	
OS	OS	Homo sapiens.	
XX	PN	US6607879-B1.	
XX	PD	19-AUG-2003.	
XX	PF	09-FEB-1998; 98US-00023655.	
XX	PR	09-FEB-1998; 98US-00023655.	
XX	PA	(INCY-) INCYTE CORP.	
XX	PI	Cocks BG, Stuart SG, Seilhamer JG;	
XX	WPI	2003-895307/82.	

XX A composition comprising a plurality of cDNAs, useful for detecting  
PT altered expression of genes in an immunological response or for  
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma  
PT or osteoarthritis.

XX Claim 1; SEQ ID NO 1475; 50pp; English.

XX The invention relates to a composition comprising a plurality of cDNAs  
CC for detecting the altered expression of genes in an immunological  
CC response. The invention also relates to a method of diagnosing or  
CC monitoring the treatment of an immunopathological condition in a sample,  
CC comprising obtaining nucleic acids from a sample, contacting the nucleic  
CC acids of the sample with an array comprising the plurality of cDNAs under  
CC conditions to form one or more hybridisation complexes, detecting the  
CC hybridisation complexes and comparing the levels of the detected  
CC hybridisation complexes with the level of hybridisation complexes  
CC detected in a non-diseased sample, where an altered level of the detected  
CC hybridisation complexes correlates with the presence of an  
CC immunopathological condition. Also disclosed are an expression profile  
CC comprising a microarray and a plurality of detectable probes. The cDNAs  
CC method for identifying a plurality of polynucleotide probes. The cDNAs  
CC are useful as hybridisable array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray can be used in  
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,  
CC ulcerative colitis, hyperesoinophilia, irritable bowel syndrome,  
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in  
CC identifying agents for the treatment of the diseases. The microarray may  
CC also be used in drug discovery and development, toxicological and  
CC carcinogenicity studies, forensics or pharmacogenomics. The composition  
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or  
CC genomic fragments. This sequence represents a human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification but was obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

Query Match 91.8%; Score 1319.2; DB 11; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAACAAAGCAATTGCCAGAAAACGTTAAGTATGGGATTTGTCTGGATGCGG 172  
DB 174 GGTTCAGCCAGAACAAAGCAATTGCCAGAAAACGTTAAGTATGGGATTTGTCTGGATGCGG 233  
QY 173 GTTCTTCTCACAAAGTTTATACATCTATAGTGGCCAGCAGAAAGGAGATGACACAG 232  
DB 234 GTTCTTCTCACAAAGTTTATACATCTATAGTGGCCAGCAGAAAGGAGATGACACAG 293  
QY 233 CGGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292  
DB 294 CGGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
QY 293 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATGTAATGAAAGAGCTAGGGAAGTGA 352  
DB 354 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATGTAATGAAAGAGCTAGGGAAGTGA 413  
QY 353 TTCCAAAGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 412  
DB 414 TTCCAAAGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 473  
QY 413 TGCTCAGGATGGAAAGTAGAAGTTGGCAGACAGAGGTTCTGGATGCTGGAGAGAGGCC 472  
DB 474 TGCTCAGGATGGAAAGTAGAAGTTGGCAGACAGAGGTTCTGGATGCTGGAGAGAGGCC 533  
QY 473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTAATCTGGCCCAAGAGGAAGTG 532  
DB 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTAATCTGGCCCAAGAGGAAGTG 593  
QY 533 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 592  
DB 594 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 653

QY 593 TCAGCATAGTCCCATATGAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTTGGGG 652  
DB 654 TCAGCATAGTCCCATATGAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTTGGGG 713  
QY 653 GAGCCTCTCACAAAGTCACTTTTGTAGCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
DB 714 GAGCCTCTCACAAAGTCACTTTTGTAGCCCAAAACAGACTATCGAGTCCCAAGATAATG 773  
QY 713 CTCTGCAATTTTGGCTCTATGCAAGGACTACAATGTCTACACATAGCTTTCTGTGCT 772  
DB 774 CTCTGCAATTTTGGCTCTATGCAAGGACTACAATGTCTACACATAGCTTTCTGTGCT 833  
QY 773 ATGGAAGGATCAGGCACTCTGGCAGAAATGGCCAAAGACATTCAGGTTGCAAGTAATG 832  
DB 834 ATGGAAGGATCAGGCACTCTGGCAGAAATGGCCAAAGACATTCAGGTTGCAAGTAATG 893  
QY 833 AAATTTCTCAGGAGCCCATCTTTCATCTCTGGATATAAGAGTAGTAGAAGTAAAGTACC 892  
DB 894 AAATTTCTCAGGAGCCCATCTTTCATCTCTGGATATAAGAGTAGTAGAAGTAAAGTACC 953  
QY 893 TTTCAAGACCCCTGACCAAGAGATTTGAGATCACTTCTCCATTTCCAGCAGTTTGAAG 952  
DB 954 TTTCAAGACCCCTGACCAAGAGATTTGAGATCACTTCTCCATTTCCAGCAGTTTGAAG 1013  
QY 953 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCTCGAGCTTTTCAACACCA 1012  
DB 1014 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCTCGAGCTTTTCAACACCA 1073  
QY 1013 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTTCGCCACACACTCCAGGGGG 1072  
DB 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTTCGCCACACACTCCAGGGGG 1133  
QY 1073 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1132  
DB 1134 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1193  
QY 1133 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1192  
DB 1194 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1253  
QY 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTCTG 1252  
DB 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTCTG 1313  
QY 1253 GTACCTACATCTCTCCCTCTTCTGCAAGGCTATCAATTCACAGCTGATTCCTGGGAGC 1312  
DB 1314 GTACCTACATCTCTCCCTCTTCTGCAAGGCTATCAATTCACAGCTGATTCCTGGGAGC 1373  
QY 1313 ACATCCCATTTTCAATTTGGCAAGATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGC 1372  
DB 1374 ACATCCCATTTTCAATTTGGCAAGATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGC 1433  
QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCA 1432  
DB 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCA 1493  
QY 1433 CCTA 1436  
DB 1494 CCTA 1497

RESULT 15

ADK60414

ID ADK60414 standard; DNA; 1818 BP.

XX

XX ADK60414;

XX AC

DT 06-MAY-2004 (first entry)

XX

DE Angiogenesis differentially expressed gene #61.

XX

KW ds; vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;

KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;  
 KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;  
 KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX FR2836687-A1.  
 XX  
 XX 05-SEP-2003.  
 XX  
 XX 11-APR-2002; 2002FR-00004546.  
 XX  
 XX 04-MAR-2002; 2002FR-00002717.  
 XX  
 XX (GENE-) GENE SIGNAL.  
 PA (ALMA/) AL MAHMOOD S.  
 XX  
 XX Colin S, Schneider C, Al Mahmood S;  
 XX  
 XX WPI; 2004-013912/02.  
 DR P-PSDB; ADK60421.  
 DR  
 XX Compositions for diagnosing, prognosing and treating angiogenic disorders  
 PT including tumor vascularization and heart disease, comprise nucleic acid  
 PT or polypeptide differentially expressed in angiogenesis.  
 XX  
 XX Claim 2; SEQ ID NO 290; 424pp; French.  
 XX  
 CC The invention relates to a novel pharmaceutical composition active on  
 CC angiogenesis comprising an endothelial cell nucleic acid whose expression  
 CC is induced by an angiogenic factor and inhibited by an angiostatic agent  
 CC or its complement or fragment, a polypeptide sequence encoded by the  
 CC nucleic acid or its fragment, a molecule capable of inhibiting expression  
 CC of the nucleic acid or a molecule which binds to the polypeptide  
 CC sequence. The invention is used to diagnose, prognose or treat an  
 CC angiogenic disorder in a mammal, particularly a human. The disorder is  
 CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,  
 CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,  
 CC endometriosis associated with neovascularization, restenosis due to  
 CC angioplasty, overproduction of tissue due to cicatrization, a peripheral  
 CC vascular disease, hypertension, vascular inflammation, Raynaud disease,  
 CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,  
 CC myocardial infarction, chronic heart disease, cardiac congestion or  
 CC macular degeneration due to age or osteoporosis. This sequence  
 CC corresponds to a differentially expressed DNA used in the composition of  
 CC the invention.  
 XX  
 SQ Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;  
 Query Match 91.8%; Score 1319, 2; DB 12; Length 1818;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 113 GTTCAACCCAGAACAAAGCATTCGAGAAACGTTAAGTATGGGATTTGCTGGATGCGG 172  
 174 GGTGACCCAGAACAAAGCATTCGAGAAACGTTAAGTATGGGATTTGCTGGATGCGG 233  
 173 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGAGAAAGGAGAAATGACACAG 232  
 234 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGAGAAAGGAGAAATGACACAG 293  
 233 GCGTGGTGCATCAAGTAGAGAAATGACGGGTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292  
 294 GCGTGGTGCATCAAGTAGAGAAATGACGGGTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
 293 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGGAAGAGCTAGGGAAGTGA 352  
 354 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGGAAGAGCTAGGGAAGTGA 413  
 353 TTCAAGGTCCTCAGCACCAGAGACACCCCGTTTACCTGGGAGCCACGGCAGGATCGGTT 412  
 414 TTCAAGGTCCTCAGCACCAGAGACACCCCGTTTACCTGGGAGCCACGGCAGGATCGGTT 473

QY 413 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGAGGTTCTGGATGTGGTGGAGAGAGCC 472  
 DB 474 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGAGGTTCTGGATGTGGTGGAGAGAGCC 533  
 QY 473 TCAGCAACTACCCCTTTGACTTCACAGGTTCCAGGATCAATTAAGTGGCCCAAGAGGAGGTG 532  
 DB 534 TCAGCAACTACCCCTTTGACTTCACAGGTTCCAGGATCAATTAAGTGGCCCAAGAGGAGGTG 593  
 QY 533 CCTATGGCTGGATTACTATCAACTACTCTGCTGGGCAAAATTCAGTGCAGAAAAACAAGTGTGT 592  
 DB 594 CCTATGGCTGGATTACTATCAACTACTCTGCTGGGCAAAATTCAGTGCAGAAAAACAAGTGTGT 653  
 QY 593 TCAGCATAGTCCCATATGAACCAATAATTCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGG 652  
 DB 654 TCAGCATAGTCCCATATGAACCAATAATTCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGG 713  
 QY 653 GAGCCTCTACAAAGTCACTTTTGTATACCCCAAAACAGACTATCGAGTCCCAGATAATG 712  
 DB 714 GAGCCTCTACAAAGTCACTTTTGTATACCCCAAAACAGACTATCGAGTCCCAGATAATG 773  
 QY 713 CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGTCT 772  
 DB 774 CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGTCT 833  
 QY 773 ATGGGAAGGATCAGGCACCTCTGCGCAAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 832  
 DB 834 ATGGGAAGGATCAGGCACCTCTGCGCAAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 893  
 QY 833 AAATTCCTCAGGACCCATGCTTTTCACTCTGGATATGAAGGTAGTGAACGTAAAGTACC 892  
 DB 894 AAATTCCTCAGGACCCATGCTTTTCACTCTGGATATGAAGGTAGTGAACGTAAAGTACC 953  
 QY 893 TTTTACAAGACCCCTGCGCAAGGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAGA 952  
 DB 954 TTTTACAAGACCCCTGCGCAAGGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAGA 1013  
 QY 953 TCCAGGGTATTGGAAATATCAACCAATGCAATCAAGACATCTCTGGAGCTTTTCAACACCA 1012  
 DB 1014 TCCAGGGTATTGGAAATATCAACCAATGCAATCAAGACATCTCTGGAGCTTTTCAACACCA 1073  
 QY 1013 GTTACTGCTTCTTACTCCAGATGCTTCAATGGGATTTTCTTGCACACACTCCAGGGGG 1072  
 DB 1074 GTTACTGCTTCTTACTCCAGATGCTTCAATGGGATTTTCTTGCACACACTCCAGGGGG 1133  
 QY 1073 ATTTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1132  
 DB 1134 ATTTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1193  
 QY 1133 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGGTTCTGTGCTCAGCTTTGGGAGG 1192  
 DB 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGGTTCTGTGCTCAGCTTTGGGAGG 1253  
 QY 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATGACTGCTTTCTG 1252  
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 DB 1314 GTACCTTACATTTCTTCCCTCTCTGCAAGGCTATCATTTTACAGCTGATTTCTGGGAGC 1373  
 QY 1313 ACATCCATTTTCTTGGCAAGATCCAGGGCAGGAGCGCGGCTGGAATTTGGGCTACATGC 1372  
 DB 1374 ACATCCATTTTCTTGGCAAGATCCAGGGCAGGAGCGCGGCTGGAATTTGGGCTACATGC 1433  
 QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCACCTCCA 1432  
 DB 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCACCTCCA 1493  
 QY 1433 CCTA 1436  
 DB 1494 CCTA 1497

Search completed: September 21, 2005, 17:05:32  
Job time : 832.224 secs

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QY 173 GTTCTTCTCACAGTTTATACATCTATAGTGGCCAGCAAGAAAGGAGATGACACAG 232
Db 248 GTTCTTCTCACAGTTTATACATCTATAGTGGCCAGCAAGAAAGGAGATGACACAG 307
QY 233 GCCTGGTGCACTCAAGTAGAAGAAATGACAGGTTAAAGTCTCGGAATCTCAAAATTTGTTTC 292
Db 308 GCCTGGTGCACTCAAGTAGAAGAAATGACAGGTTAAAGTCTCGGAATCTCAAAATTTGTTTC 367
QY 293 AGAAAGTAATGAAATAGGCAATTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 352
Db 368 AGAAAGTAATGAAATAGGCAATTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 427
QY 353 TTCCAGGTCGCCAGCACAGACACCCGTTTACCTGGGAGCCAGCGGAGGATCGCGGT 412
Db 428 TTCCAGGTCGCCAGCACAGACACCCGTTTACCTGGGAGCCAGCGGAGGATCGCGGT 487
QY 413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGAGGTTCTGGATGTGGTGAGAGGAGCC 472
Db 488 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGGTGAGAGGAGCC 547
QY 473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATATTCTGGCCAAAGAGGAAAGGTG 532
Db 548 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATATTCTGGCCAAAGAGGAAAGGTG 607
QY 533 CCTATGGCTGATTAATCAATCTATCTGCTGGCCAAATTCAGTCAGAAAACAAGGTGCT 592
Db 608 CCTATGGCTGATTAATCAATCTATCTGCTGGCCAAATTCAGTCAGAAAACAAGGTGCT 667
QY 593 TCAGCATAGTCCCATATGAAACCAATAATCAGAAAACCTTTGGAGCTTTGGACTTTGGGG 652
Db 668 TCAGCATAGTCCCATATGAAACCAATAATCAGAAAACCTTTGGAGCTTTGGACTTTGGGG 727
QY 653 GAGCCTCTACACAAGTCATTTTGTATCCCCAAACCCAGACTATCGAGTCCCAAGATAATG 712
Db 728 GAGCCTCTACACAAGTCATTTTGTATCCCCAAACCCAGACTATCGAGTCCCAAGATAATG 787
QY 713 CTCTGCATTTCCGCTCTATGSCAAGGACTTACATCTCTACACATAGCTTCTTGCT 772
Db 788 CTCTGCATTTCCGCTCTATGSCAAGGACTTACATCTCTACACATAGCTTCTTGCT 847
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QY 1013 GTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTTCTGCGCAACCACTCCAGGGG 1072
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DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX436692
VERSION BX436692.2 GI:47007879
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 984)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30779500.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5524.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CS0CAP003AF11QPI&c=5524.f.
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Library was not normalized."
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## ORIGIN

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Matches 949; Conservative 12; Mismatches 7; Indels 1; Gaps 1;

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QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGATGACACAG 232
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ORIGIN

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Query Match      60.1%; Score 863; DB 3; Length 2410;
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QY 224 ACCGAGCAACAAACCTTTCGCAAGAAATGTTAAGTATGGGATTCGCTGGATCGGGTCA 283
DB 224 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB 178 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB 284 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB 404 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB 358 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB 464 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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ACCESSION AK030601
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REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
2
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

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TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159  
3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861  
4

TITLE  
JOURNAL  
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AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5

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JOURNAL  
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PUBMED  
REFERENCE  
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 4198)

TITLE  
JOURNAL  
MEDLINE  
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REFERENCE  
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
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Muramatsu, M. and Hayashizaki, Y.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.

FEATURES  
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REFERENCE	1	Carninci, P. and Hayashizaki, Y.											
AUTHORS	High-efficiency full-length cDNA cloning												
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JOURNAL	99279253												
MEDLINE	10349636												
PUBMED													
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.											
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes												
TITLE	Genome Res.	10 (10), 1617-1630 (2000)											
JOURNAL	20499374												
MEDLINE	11042159												
PUBMED													
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.											
AUTHORS	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer												
TITLE	Genome Res.	10 (11), 1757-1771 (2000)											
JOURNAL	20530913												
MEDLINE	11076861												
PUBMED													
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.											
AUTHORS	Functional annotation of a full-length mouse cDNA collection												
TITLE	Nature	409, 685-690 (2001)											
JOURNAL													
MEDLINE													
PUBMED													
REFERENCE	5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.											
AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs												
TITLE	Nature	420, 563-573 (2002)											
JOURNAL													
MEDLINE													
PUBMED													
REFERENCE	6	(bases 1 to 3563)											
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shitaki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.												
TITLE	Direct Submission												

JOURNAL	Submitted (16-JUL-2001) Yoshitake Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.
FEATURES	Location/Qualifiers
Source	1. 3563 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM.DB:4732419M16" /clone="4732419M16" /tissue_type="skin" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="10 days neonate" <1. 1265 /note="unnamed protein product; ectonucleoside triphosphate diphosphohydrolase 1 (MGD MG1:102805, GB NM_009848, evidence: BLASTN, 100%, match=2284), putative" /codon_start=3 /protein_id="BAC26037.1" /db_xref="GI:26324566" /translation="ISKVAQKTEIGAYLAECWELSTELIPTSKHQTPTVVLGATAG RLNLSEQSADEVLAAYVSLKSYFDFFQGAIIITQBEAGYAGWITINYLILGRTFT QSWLISLDSQKQTFGALDGGASTQITFPQNSTISEPNSLOFLRYLGDYTYTH PFCQKQDQALWQKLAKDIQVSSGVLKDFCPNGYKVVNVSELYGTPCTKREKKI SFDQFRQTGQDLEIQHQSILELFPNNSHCYPSOCAPNGVLPPLHGSFGAPSAFYFM DFRKKVAKNSVISQEKMTETKNCFSKSWETKTSYPSVKEKLYSEYCFSGAYLISLL QGYNFTSSVMEQHPMGKI KDSNAGWTLCYMLNLTNNIPAEQPLSPPLPSTYIGLMV LFSLLGVAAITGLFIYSKFSYFWEAV"
CDS	polyA_signal 3542..3547 /note="putative" polyA_site 3563 /note="putative" ORIGIN
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Best Local Similarity	79.2%; Pred. No. 9.8e+208;
Matches	924; Conservative 0; Mismatches 231; Indels 12; Gaps 3;
Qy	276 AATCTCAAAATTTGTTTCAGAAAGTAATGAATGAATAGGCATTTACCTGACTGATTCATGGA 335
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Qy	336 AAGAGCTAGGGAAGTGTATCCAGGTCCTCAGACCAAGACACCCGCTTTACCTGGGAGC 395
Db	62 ACTGTCCACCGAAGTGTATCAACATCCAGCATCCAGAGCTCTCTGTACCTGGGAGC 121
Qy	396 CACGGCAGGCATCGGTTGCTCAGGATGGAAGAGTGTGCGACAGAGGGTTCCTGGA 455
Db	122 CACAGCAGGCATCGCTTGTCTTAGAATGGAAGAGCAACATCGGCAGACCGAGGTCCTGGC 181
Qy	456 TGTGTGTGAGAGGAGCCTCAGCAACTACCCCTTTGACTTCCAGGTCGCGAGGATCATATAC 515
Db	182 TGCAGTGTCAACAGCGCTTAAGAGCTACCCCTTTGACTTCCAGGTCGCGAGGATCATCAC 241
Qy	516 TGGCCACAGAGAGGTCCTGTATGCTGCTGATCTATCAACTATCTGCTGCGCAAAATTCAG 575
Db	242 TGGACACAGAGAGGTCCTGTATGCTGCTGATCTATCAACTATCTGCTGCGCAAGATTCAC 301
Qy	576 TCAGAAAACAAAGGTGTTTCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGG 635





QY	713	CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGCTTACACACATAGCTTCTTGCT	772
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QY	773	ATGGGAAGGATCAGGACACTCTGGCGAAGAACTGGCCCAAGGACATTTCAGGTTGCAAGTAATG	832
Db	831	ATGGGAAGGATCAGGACACTCTGGCGAAGAACTGGCCCAAGGACATTTCAGGTTGCAAGTAATG	890
QY	833	AAATCTCAGGGACC	847
Db	891	AAATCTCAGGGACC	905
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LOCUS			
DEFINITION			
AGENCOURT_6621802 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724619			
5', mRNA sequence.			
ACCESSION			
BM906668			
VERSION			
BM906668.1 GI:19357047			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>			
Tissue Procurement: Invitrogen			
cDNA Library Preparation: Life Technologies, Inc.			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
<a href="http://image.llnl.gov">http://image.llnl.gov</a>			
Plate: LLM12714 row: c column: 20			
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High quality sequence stop: 664.			
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Site1: EcoRV (destroyed); Site2: NotI; RNA source pool			
of three ovaries, from females ranging in age from 38 to			
49 yo. Library is oligo-dT primed and directionally cloned			
(EcoRV site is destroyed upon cloning). Average insert			
size 2.1 kb, insert size range 1-3.5 kb. Library is			
normalized and enriched for full-length clones and was			
constructed by C. Gruber (Invitrogen). Research Genetics			
tracking code 036."			
source			
ORIGIN			
Query Match			
50.6%; Score 727; DB 5; Length 1066;			
Best Local Similarity			
93.6%; Pred. No. 4.6e-203;			
Matches 825; Conservative			
0; Mismatches 45; Indels 11; Gaps 6;			
QY	113	GTTCAACCCAGAACAGCAATTCGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG	172
Db	185	GTTGACCCAGAACAAAGCAATTCGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG	244
QY	173	GTTCTTCTCACAGATTATACATCTATAAGTGGCCAGCAGAAAGGAGAAATGACACAG	232
Db	245	GTTCTTCTCACAGATTATACATCTATAAGTGGCCAGCAGAAAGGAGAAATGACACAG	304

QY	223	CGCTGGTGCATCAAGTAGAAGATCGAGGTTAAAGGCTCTCGAAATCTCAAAATTTGTTTC	292
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QY	293	AGAAAGTAATGAATAGCATTTTACCTGACTGATTCGATGCAAGAGAGCTAGGAGATGA	352
Db	365	AGAAAGTAATGAATAGCATTTTACCTGACTGATTCGATGCAAGAGAGCTAGGAGATGA	424
QY	353	TTCCAAAGGTCCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCGATCGGT	412
Db	425	TTCCAAAGGTCCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCGATCGGT	484
QY	413	TGCTCAGGATGGAAGTGAAGTTGGCAGACAGGGTTCTCGATGTGTGGAGAGAGCC	472
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QY	473	TCAGCAACTACCCCTTTCGACTTCCAGGGTGCAGGATCATTTACTGGCCAAAGGAGGTG	532
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QY	593	TCAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG	652
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QY	653	GAGCTCTACACAGTCACTTTTGTACCCCAAAACCACTATCAGTCCCGCCAGATAATG	712
Db	725	GAGCTCTACACAGTCACTTTTGTACCCCAAAACCACTATCAGTCCCGCCAGATAATG	784
QY	713	CTCTGCAATTTCCGCTCTATGCGCAAGGACTACAATGTCTACACACATAGCTTCTTGCTGT	772
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QY	831	TGAATTTCTCAGGACCCATGC- TTTTCATCTCGATATAGAGGTAGTGAACGTAA- 886	
Db	905	TGAATTTCTCAGGACCCATGC- TTTTCATCTCGATATAGAGGTAGTGAACGTAAAG	964
QY	887	-GTGACCTTTTACAAGACCCCTGCAACCAAGAGATTGAGTGAATCTTCCATT- -CCAGC	943
Db	965	GGACCTTTACAAGAACCCCTGCAACCAAAATTTGAGAGACTCTTCTTCTTCCCCNA	1024
QY	944	AGTTTGAAT- -CCAGGATTTGGAACATATCAACAATGCC	982
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DEFINITION	AL552123 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA		
ACCESSION	AL552123		
VERSION	AL552123.3	GI:45856912	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 897)			
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.			
Full-length cDNA libraries and normalization			
Unpublished (2001)			
On Feb 15, 2001 this sequence version replaced gi:31273939.			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			



Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5524.f

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DI059A806QP1&c=5524.f.

FEATURES  
source

Location/Qualifiers  
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/organism="Homo sapiens"  
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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6  
vector. Library was normalized."

ORIGIN

Query Match 50.1%; Score 720.6; DB 1; Length 897;  
Best Local Similarity 94.3%; Pred. No. 3.4e-201;  
Matches 765; Conservative 13; Mismatches 28; Indels 5; Gaps 3;  
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Qy 173 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 232  
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Qy 353 TTCAGAGTCCCGACACAGACACCCGTTTACCTGGGAGCCAGCGGATCGGT 412  
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Qy 653 GAGCCTCTACACAGTCACTTTTGTATCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
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Qy 713 CTCTGCAATTTGCGCTTATGGCAAGCACTACATGCTTACACATAGCTTCTTGCT 772  
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Db 750 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAGGACATTCAGGTTGCAAGTAATG 812

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Qy 893 TTTACAAGACCCCTGCGACCAAGAGATTGA 923  
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RESULT 10  
BX402316

LOCUS  
DEFINITION

ACCESSION  
VERSION

KEYWORDS  
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX402316 1025 bp mRNA linear EST 28-APR-2004  
BX402316 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0DI017YB13 5-PRIME, mRNA sequence.  
BX402316  
BX402316 GI:46844926  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 13, 2003 this sequence version replaced gi:30610946.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5524.f

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS1A10052B07QP1&c=5524.f.  
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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6  
vector. Library was normalized."

FEATURES  
source

Query Match 48.9%; Score 702.2; DB 5; Length 1025;  
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Matches 704; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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Db 248 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 307  
Qy 233 GCGTGGTGCACTCAAGTAGAAGATTCAGGTTAAAGCTCTGGAATCTCAAAATTTGTTTC 292  
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ORIGIN

Query Match 48.9%; Score 702.2; DB 5; Length 1025;  
Best Local Similarity 99.6%; Pred. No. 9.9e-196;  
Matches 704; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 113 GTTCAACCCAGACAAAGCATTTGCCAGAAAACGTTAAGTATGGATTGCTGGATGCGG 172  
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Qy 173 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 232  
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Qy 233 GCGTGGTGCACTCAAGTAGAAGATTCAGGTTAAAGCTCTGGAATCTCAAAATTTGTTTC 292  
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Qy 293 AGAAAGTAATGAATAGGCAATTTACTGACTGATTCGATGGAAGAGCTAGGGAAGTGA 352  
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488 TGCTCAGGATGGAAGTGAAGTGGCCAGACAGGGTTCTGGATGTTGGAGAGAGCC 547  
473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAATGAGGAGAGAGGTTG 532  
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533 CCTATGGCTGGATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 592  
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RESULT 11  
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LOCUS  
DEFINITION  
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clone CS0D1017YB13 5-PRIME, mRNA sequence.  
ACCESSION  
AL547722  
VERSION  
AL547722.3 GI:45748162  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1023)  
AUTHORS  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished (2001)  
COMMENT  
On Feb 15, 2001 this sequence version replaced gi:31369551.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE  
Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5524.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CS0D1017CA07QPI&c=5524.f.  
Location/Qualifiers  
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/note="1st strand cDNA was primed with a NotI-oligo (dT)  
primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match  
Best Local Similarity 48.5%; Score 697.6; DB 1; Length 1023;  
Matches 697; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 113 GTTCAACCCAGAACCAAGCATTTGCCAGAAACGTTTAAGTATGCGGATTTGCTGGATGCGG 172  
DB 198 GGTTCACCCAGAACCAAGCATTTGCCAGAAACGTTTAAGTATGCGGATTTGCTGGATGCGG 247  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGAGAAAGAGAAATGACACAG 232  
DB 248 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGAGAAAGAGAAATGACACAG 307  
QY 233 GCGTGGTGCATCAAGTAGAAGATTCAGAGGTTTAAAGGTCCTGGATCTCAAAATTTGTTTC 292  
DB 308 GCGTGGTGCATCAAGTAGAAGATTCAGAGGTTTAAAGGTCCTGGATCTCAAAATTTGTTTC 367  
QY 293 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGCGGAAGTGA 352  
DB 368 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGCGGAAGTGA 427  
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clone CS0D107YD08 5-PRIME, mRNA sequence.  
ACCESSION  
BX327984  
VERSION  
BX327984.1 GI:30332721  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 952)  
AUTHORS  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished (2001)



Db 352 CTGGGCAATTCAGTCAGAAAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAAT 411

Qy 622 CAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTGTACCC 681

Db 412 CAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTGTACCC 471

Qy 682 CAAAAACAGACTATCAGATCCCAAGATATGCTCTGCAATTTGCGCTCTATGSCAAGGAC 741

Db 472 CAAAAACAGACTATCAGATCCCAAGATATGCTCTGCAATTTGCGCTCTATGSCAAGGAC 531

Qy 742 TACAATGTCTACACATAGCTTTCTGTGCTATGGAAGGATCAGGACCTCTGGCAGAA 801

Db 532 TACAATGTCTACACATAGCTTTCTGTGCTATGGAAGGATCAGGACCTCTGGCAGAA 591

Qy 802 CTGGCCAAAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTTTCATCCT 861

Db 592 CTGGCCAAAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTTTCATCCT 651

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Db 652 GGNATATAAGAGTAGTGAACGTAAAGTAGCTTTTACAGACCCCTTGACCAAGATTT 711

Qy 922 GAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGGAACCTATCAACAATGC 981

Db 712 GAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGGAACCTATCAACAATGC 771

Qy 982 CATCAAAGCATCTCGAGCTCTTCAACACAGTTACTGCGCTTTACTCCCTCC-AGTGTGCTTT 1040

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Qy 1096 TACTTTGTGATGAGTTT--AACTTGCATCAGAG-NAAGTCTTCAAGGAAAGG--T 1151

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ACCESSION BF664417 GI:11938222  
VERSION EST.  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 808)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-romail.nih.gov](mailto:cgapbs-romail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1183 row: n column: 16  
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Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 44.9%; Score 645.2; DB 2; Length 808;  
Best Local Similarity 98.7%; Pred. No. 6.6e-179;  
Matches 693; Conservative 0; Mismatches 3; Indels 6; Gaps 4;

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Db 62 AAGGACTACAATGTCTACACATAGCTTTTGTGCTATGGGAAGGATCAGGCACCTCTCG 121

Qy 796 CAGAACTGGCCAAAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTT 855

Db 122 CAGAACTGGCCAAAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTT 181

Qy 856 CATCTGATATAGAAGGTAGTGAACCTTGAATCCAGGGTATTTGGAACCTATCAAA 915

Db 182 CATCTGATATAGAAGGTAGTGAACCTTGAATCCAGGGTATTTGGAACCTATCAAA 241

Qy 916 AGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGGAACCTATCAA 975

Db 242 AGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGGAACCTATCAA 299

Qy 976 CAATGCCATAAAGCATCTCGAGCTTTCAACACAGTTACTGCGCTTTACTCCAGTGT 1035

Db 300 CAATGCCATAAAGCATCTCGAGCTTTCAACACAGTTACTGCGCTTTACTCCAGTGT 359

Qy 1036 GCCTTCAATGGGATTTCTGCCACCCTCCAGGGGATTTTGGGGCATTTTCAGCTTT 1095

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Qy 1096 TACTTTGTGATGAAGTTTAAACCTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACT 1155

Db 418 TAC--TTGTGATGAAGTTTAAACCTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACT 476

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Db 477 GAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATATAAACAATCTTACCTGGA 536

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Db 537 GTAAGGAGAGTACCTGAGTGAATCTGCTTTTCTGTGCTACATCTCTCCCTCCTT 596

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Db 597 CTGCAAGGCTATCATTTTCAACAGCTGATTTCTCGGAGACATCCATTTTCA--TGGCAAGATC 655

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Db 656 CAGGGCAGCAGCGCGCTGGACTTTTGGGCTTACATGCTGAAC 697

RESULT 15  
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LOCUS CB553295 673 bp mRNA linear EST 01-JUN-2003

DEFINITION	MMSP0076 A03 MMSP Macaca mulatta cdNA, mRNA sequence.
ACCESSION	CB553295
VERSION	CB553295.1 GI:31302490
KEYWORDS	Esf.
SOURCE	Macaca mulatta (rhesus monkey)
ORGANISM	Macaca mulatta
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
TITLE	Cercopitheciae; Macaca.
JOURNAL	1 (bases 1 to 673)
COMMENT	Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and Holzman, T.
FEATURES	Expressed sequence tags from Rhesus macaque spleen
source	Unpublished (2002)
	Contact: Holzman T
	Katze Lab
	University of Washington
	Box 358070, Seattle, WA 98195-8070, USA
	Tel: 206 732 6156
	Fax: 206 732 6055
	Email: ted@locke.hi.washington.edu
	Similar to GenBank entry S73813 S73813 CD39=lymphoid cell
	activation antigen [human, B lymphoblastoid cell line, MP-1, mRNA,
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Search completed: September 21, 2005, 23:22:06	
Job time : 5136.07 secs	

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	463.2	32.2	871	4	US-09-949-016-2106
5	291	20.3	2782	4	US-09-949-016-5457
6	291	20.3	2797	3	US-09-240-639-3
7	291	20.3	2797	4	US-09-908-510A-3
8	291	20.3	2797	4	US-09-905-744B-3
9	291	20.3	2797	4	US-10-107-660-3
10	291	20.3	2797	4	US-10-107-576-3
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16	245.8	17.1	601	4	US-09-949-016-71601
17	220.8	15.4	1500	4	US-09-949-016-5688
18	167.8	11.7	364	4	US-09-513-999C-196
19	167	11.6	601	4	US-09-949-016-71600
20	140.4	9.8	601	4	US-09-949-016-71607
21	139	9.7	742	2	US-08-966-316-2
22	108	7.5	4928	1	US-08-345-913-1
23	108	7.5	4928	3	US-08-818-562-1
24	108	7.5	4928	3	US-08-628-445-1
25	108	7.5	5552	3	US-08-155-888-1
26	108	7.5	5585	2	US-08-303-221-1
27	108	7.5	5585	4	US-09-000-003A-1

ALIGNMENTS

RESULT 1

US-08-930-921-2  
; Sequence 2, Application US/08930921B  
; Patent No. 6287837  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; APPLICANT: SEVIGNY, Jean  
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN  
; CURRENT APPLICATION NUMBER: US/08/930,921B  
; CURRENT FILING DATE: 1998-01-02  
; EARLIER APPLICATION NUMBER: PCT/CA96/00223  
; EARLIER FILING DATE: 1996-04-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: unknown  
US-08-930-921-2

Query Match	91.8%	Score 1319.2;	DB 3;	Length 1818;
Best Local Similarity	99.8%	Pred. No. 0;		
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 1253 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGCTGATTTCTCGGAGC 1312  
 1314 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGCTGATTTCTCGGAGC 1373  
 1313 ACATCCATTTTCATTTGGCAAGATCCAGGCGACGACGCGGCTGGACTTTGGGCTACATGC 1372  
 1374 ACATCCATTTTCATTTGGCAAGATCCAGGCGACGACGCGGCTGGACTTTGGGCTACATGC 1433  
 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCACACCTCTCTCCACTCCA 1432  
 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCACACCTCTCTCCACTCCA 1493  
 1433 CCTA 1436  
 1494 CCTA 1497

US-09-023-655-1475  
 ; Sequence 1475, Application US/09023655  
 ; Patent No. 6607879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/023,655  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1475:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1818 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: 9765255  
 ; US-09-023-655-1475

Query Match 91.8%; Score 1319.2; DB 4; Length 1818;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 113 GTTCAACCCAGAACAAAGCAATTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATGCGG 172  
 DB 174 GGTGACCCAGAACAAAGCAATTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATGCGG 233  
 QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGAAATGACACAG 232  
 DB 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGAAATGACACAG 293  
 QY 233 GCGTGGTGATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 292  
 DB 294 GCGTGGTGATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 353  
 QY 293 AGAAAGTAAATGAAATAGGCATTTTACCTGACATGATTTGATGATGAAAGAGCTTAGGGAAAGTGA 352  
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 QY 353 TTCCAGGTCCCGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGATCGCTCGGT 412  
 DB 414 TTCCAGGTCCCGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGATCGCTCGGT 473  
 QY 413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTTGGATGTGTGGAGAGGAGCC 472



Db 474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTCTGGATGTGGTGGAGAGAGCC 533  
 Qy 473 TCAGCAACTACCCCTTTGACTTCACGGGTGCCAGGATCATTTACTTGCCCAAGGAAGGTG 532  
 Db 534 TCAGCAACTACCCCTTTGACTTCACGGGTGCCAGGATCATTTACTTGCCCAAGGAAGGTG 593  
 Qy 533 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 592  
 Db 594 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 653  
 Qy 593 TCAGCATAGTCCCATATGAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTGGGG 652  
 Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTGGGG 713  
 Qy 653 GAGCCTCTACAAAGTCACCTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
 Db 714 GAGCCTCTACAAAGTCACCTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 773  
 Qy 713 CTCTGCAATTTGCGCTCTATGGCAAGGATCAAAATGTCTACACATAGCTTTCTGTGT 772  
 Db 774 CTCTGCAATTTGCGCTCTATGGCAAGGATCAAAATGTCTACACATAGCTTTCTGTGT 833  
 Qy 773 ATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCCAAGGACATTCAGGTGCAAGTAATG 832  
 Db 834 ATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCCAAGGACATTCAGGTGCAAGTAATG 893  
 Qy 833 AAATTCCTCAGGACCCCATCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTACC 892  
 Db 894 AAATTCCTCAGGACCCCATCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTACC 953  
 Qy 893 TTTTACAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCCATTCACAGCAGTTTGAAA 952  
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 Db 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGGAGG 1253  
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 Db 1254 AGATAAAAACATCTTACGCTGAGTAAAGGAGAAGTACTGAGTGAATCTGCTTTTCTG 1313  
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 Db 1314 GPACCTACATTTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTCCTGGGAGC 1373  
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 Db 1374 ACATCCATTTCAATGGCAAGATCCAGGGCAGGACCGCGGTGGACTTTGGGCTACATGC 1433  
 Qy 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCACTTGTCACACCTCTCTCCCACTCCA 1432  
 Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCACTTGTCACACCTCTCTCCCACTCCA 1493  
 Qy 1433 CCTA 1436  
 Db 1494 CCTA 1497

US-09-781-796C-2  
 ; Sequence 2, Application US/09781796C  
 ; Patent No. 6800284  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BEAUDOIN, Adrien R.  
 ; APPLICANT: SEVIGNY, Jean  
 ; APPLICANT: BACH, Fritz H.  
 ; APPLICANT: ROBSON, Simon  
 ; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
 ; THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
 ; TITLE OF INVENTION: TECHNOLOGY  
 ; FILE REFERENCE: 920333.90019  
 ; CURRENT APPLICATION NUMBER: US/09/781,796C  
 ; CURRENT FILING DATE: 2001-02-12  
 ; PRIOR APPLICATION NUMBER: 08/419,204  
 ; PRIOR FILING DATE: 1995-04-10  
 ; PRIOR APPLICATION NUMBER: CA96/00223  
 ; PRIOR FILING DATE: 1996-04-10  
 ; PRIOR APPLICATION NUMBER: 08/930,921  
 ; PRIOR FILING DATE: 1998-02-01  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1818  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-781-796C-2

Query Match 91.8%; Score 1319.2; DB 4; Length 1818;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAACGTTTAAGTATGGGATTTGCTGGATGCCG 172  
 Db 174 GGTGACCCAGAACAAAGCATTTGCCAGAAAAACGTTTAAGTATGGGATTTGCTGGATGCCG 233  
 Qy 173 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGAGAAATGACACAG 232  
 Db 234 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGAGAAATGACACAG 293  
 Qy 233 CGTGGTGCATCAAGTAGAAGTTCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292  
 Db 294 CGTGGTGCATCAAGTAGAAGTTCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
 Qy 293 AGAAAGTAAATGAATAGGCAATTTACCTGATTTGATTCATGGAAGAGCTAGGGAAGTGA 352  
 Db 354 AGAAAGTAAATGAATAGGCAATTTACCTGATTTGATTCATGGAAGAGCTAGGGAAGTGA 413  
 Qy 353 TTCCAAGGTCCCAAGCAGCAACCCGTTTACCTGGAGCCACCGCATGCCGATGCCGT 412  
 Db 414 TTCCAAGGTCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 473  
 Qy 413 TGCTCAGATGGAAAGTGAAGTTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGG 472  
 Db 474 TGCTCAGATGGAAAGTGAAGTTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGG 533  
 Qy 473 TCAGCAACTACCCCTTTGACTTCAGGGTGCAGGATCATTTACTGGCCAAAGGAAGGTG 532  
 Db 534 TCAGCAACTACCCCTTTGACTTCAGGGTGCAGGATCATTTACTGGCCAAAGGAAGGTG 593  
 Qy 533 CCTATGGCTGGATTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 592  
 Db 594 CCTATGGCTGGATTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 653  
 Qy 593 TCAGCATAGTCCCATATGAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTGGGG 652  
 Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTGGGG 713  
 Qy 653 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
 Db 714 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 773  
 Qy 713 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTGTGTCT 772

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Db 774 CTCTGCAATTTCCGCTCTATGGCAAGGACTACATGCTACACACATAGCTTCTGTGCT 833
Qy 773 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832
Db 834 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893
Qy 833 AATTTCTCAGGACCCATGCTTTCATCCCTGGATATAGAGGAGTAGAACGTAAGTGACC 892
Db 894 AATTTCTCAGGACCCATGCTTTCATCCCTGGATATAGAGGAGTAGAACGTAAGTGACC 953
Qy 893 TTTTACAAGACCCCTTCACCAAGAGATTTTGAGATGACTCTTTCATTTCCAGCAGTTTGAAA 952
Db 954 TTTTACAAGACCCCTTCACCAAGAGATTTTGAGATGACTCTTTCATTTCCAGCAGTTTGAAA 1013
Qy 953 TCAGGGTATGTGAAACTATCAACAATGCCATCAAAAGCATCTCGAGAGCTTCCAAACCA 1012
Db 1014 TCCAGGGTATGTGAAACTATCAACAATGCCATCAAAAGCATCTCGAGAGCTTCCAAACCA 1073
Qy 1013 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1072
Db 1074 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1133
Qy 1073 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1132
Db 1134 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1193
Qy 1133 AAGTCTCTCAGGAAAGGAGTCTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG 1192
Db 1194 AAGTCTCTCAGGAAAGGAGTCTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG 1253
Qy 1193 AGATTAACACATCTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTCTG 1252
Db 1254 AGATTAACACATCTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTCTG 1313
Qy 1253 GTACCTACATCTCTCCTCTCTCAAGGCTATCATTTTCAAGCTGATTTCTCTGGGAGC 1312
Db 1314 GTACCTACATCTCTCCTCTCTCTGCAAGGCTATCATTTCAAGCTGATTTCTCTGGGAGC 1373
Qy 1313 ACATCAATTTCAATGGCAAGATCCAGGCGACGACGCGCGCTGGACTTTGGGGTACATGC 1372
Db 1374 ACATCAATTTCAATGGCAAGATCCAGGCGACGACGCGCGCTGGACTTTGGGGTACATGC 1433
Qy 1373 TGAACCTGACCAATGATCCGAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA 1432
Db 1434 TGAACCTGACCAATGATCCGAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA 1493
Qy 1433 CCTA 1436
Db 1494 CCTA 1497

RESULT 4
US-09-949-016-2106
; Sequence 2106, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2106
; LENGTH: 871

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106
Query Match 32.2%; Score 463.2; DB 4; Length 871;
Best Local Similarity 99.4%; Pred. No. 6.7e-144;
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 113 GTTCAACCCAGAACCAAGCATTTGCCAGAAAAGCTTAAGTATATGGATTTGCTGGATGCCG 172
Db 198 GGTTCACCCAGAACCAAGCATTTGCCAGAAAAGCTTAAGTATATGGATTTGCTGGATGCCG 257
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATACTATACTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 232
Db 258 GTTCTTCTCACACAAGTTTATACATCTATACTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 317
Qy 233 GCGTGGTGATCAAGTAGAAGAAATCAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTC 292
Db 318 GCGTGGTGATCAAGTAGAAGAAATCAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTC 377
Qy 293 AGAAAGTAATAAATAGGATTTACCTGACTGATTTGATGCAATGCAAGAGCTAGGGAAGTCA 352
Db 378 AGAAAGTAATAAATAGGATTTACCTGACTGATTTGATGCAATGCAAGAGCTAGGGAAGTCA 437
Qy 353 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCAGCGCATGCGGT 412
Db 438 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCAGCGCATGCGGT 497
Qy 413 TGCTCAGGATGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGAGGCC 472
Db 498 TGCTCAGGATGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGAGGCC 557
Qy 473 TCAGCAACTACCCCTTGACTTCCAGGGTGCCAGGATCATTTACTGCCAAGAGGAGGTG 532
Db 558 TCAGCAACTACCCCTTGACTTCCAGGGTGCCAGGATCATTTACTGCCAAGAGGAGGTG 617
Qy 533 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGA 580
Db 618 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGA 665

RESULT 5
US-09-949-016-5457
; Sequence 5457, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5457
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5457
Query Match 20.3%; Score 291; DB 4; Length 2782;
Best Local Similarity 54.3%; Pred. No. 7e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;
Qy 120 CCAGAACAAAGCATTTGCCAGAAAAGCTTAAGTATGGAATTTGCTGGATGCCGGTTCTTC 179
Db 219 CAAGCAAGAGGTCTCCCTCCAGGAGTGAAGTATGATTTGCTGGATGCCGGTTCTTC 278
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Db 774 CTCTGCAATTTCCGCTCTATGGCAAGGACTACATGCTACACACATAGCTTCTGTGCT 833
Qy 773 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832
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Qy 833 AATTTCTCAGGACCCATGCTTTCATCCCTGGATATAGAGGAGTAGAACGTAAGTGACC 892
Db 894 AATTTCTCAGGACCCATGCTTTCATCCCTGGATATAGAGGAGTAGAACGTAAGTGACC 953
Qy 893 TTTTACAAGACCCCTTCACCAAGAGATTTTGAGATGACTCTTTCATTTCCAGCAGTTTGAAA 952
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Qy 953 TCAGGGTATGTGAAACTATCAACAATGCCATCAAAAGCATCTCGAGAGCTTCCAAACCA 1012
Db 1014 TCCAGGGTATGTGAAACTATCAACAATGCCATCAAAAGCATCTCGAGAGCTTCCAAACCA 1073
Qy 1013 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1072
Db 1074 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1133
Qy 1073 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1132
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Db 1314 GTACCTACATCTCTCCTCTCTCTGCAAGGCTATCATTTCAAGCTGATTTCTCTGGGAGC 1373
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Qy 1373 TGAACCTGACCAATGATCCGAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA 1432
Db 1434 TGAACCTGACCAATGATCCGAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA 1493
Qy 1433 CCTA 1436
Db 1494 CCTA 1497

RESULT 4
US-09-949-016-2106
; Sequence 2106, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2106
; LENGTH: 871
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QY 180 TCACACAGTTTATACATCTATAAGTGGCCAGCAGAGAAAGGAGAATGACACAGGGGTGT 239  
DB 279 AAGAACCACAGTCTACGTGTATCAATGGCCAGCAGAGAAAGGAGAATAATACCGGAGTGT 338  
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QY 360 GTCCAGCAGCAAGAGACACCCGTTTACCTGGGAGCCAGGCGAGCATGCGGTTCCTCAG 419  
DB 459 CCACCTCCACGATCCACCCCAATTCACCTGGGAGCCAGGCTGGGATGCGCTTCTGAG 518  
QY 420 GATGAAAGTGAAGATTTGGCAGACAGGGTTCTGATGCTGGTGGAGAGGCTTCAGCA 479  
DB 519 GTTGCAAAATGAACAGCAGCTTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC 578  
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QY 600 AGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGAGGCTC 659  
DB 699 GGTGC-----ACCCGCAATGGAGTGGAAACCAACGGGTGCCCTGGACTTAGGTGGTGCCTC 752  
QY 660 TACAAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATGCTCTGCA 719  
DB 753 CACCAAAATATCTTCGTGGCAGGAGAGAGATGATCTGAACACAGGACATCATGCA 812  
QY 720 ATTTCGCTTATGCGAAGGACTACAATGCTCTACACATAGCTTTCTTGTCTATGGAA 779  
DB 813 GGTGTCCCTGTATGCTACGTATACACGCTCTACACACAGCTTCCAGTGTCTATGGCG 872  
QY 780 GGATCAGCAGCTCTGGCAGAACTGGCCAGACATTCAGGTTCGAAATGAA---T 836  
DB 873 GAAAGAGCTGAGAAGAGTTCCTGCAATGCTCTCGCAGAAATCTCTCTACCAAAACCA 932  
QY 837 TCTCAGGACCCATCTTTCATCTCGGATATAAGAAAGGTAGTGAACGTAAAGTACCTTTA 896  
DB 933 TCTCACCATCTCTTACCTCGGATATAGCATCAGCTTCACCATGGGCCATGTATT 992  
QY 897 CAAGACCCCTGCAC-----CAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTGA 950  
DB 993 TGATAGCCTGTGCACTGTGGACAGAGCCAGAGAAAGTTATAACCCCAATGATGTCATCAC 1052  
QY 951 AATCCAGGGTATGGAACATATCAACATGCCATCAAGCATCTCGGAGCTTCTCAACAC 1010  
DB 1053 TTTTGAAGGAACTGGGGACCCATCTCTGTGTAAGGAGAGGTGGCTTCCATATTGACTT 1112  
QY 1011 CAGTTACTGCTTACTCCAG---TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCA 1067  
DB 1113 CAAGCTTGCATGATCAAGAAACCTGTTCTTTGATGGGTTTATCAGCCAAAGATTAA 1172  
QY 1068 GGGGATTTGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAAACTTTGACATC 1127  
DB 1173 AGGGCAATTTGGGCTTTTGGCAGGATTTACTTACACAGCCAGTGCTTTTAAATCT---TTC 1229  
QY 1128 AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGTCTGTGCTCAGCCTTG 1187  
DB 1230 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGGAAATTTCTGCTCACAGAATTG 1289  
QY 1188 GGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTT 1247  
DB 1290 GAGTCAGCTCCACTGCTCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT 1349

QY 1248 TTCTGGTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTCAGAGCTGATTCCTG 1307  
DB 1350 CTCAGCCAACTACATCTACCACTTTGTTGTGAACGGTTACAAATTCACAGAGGAGACTTG 1409  
QY 1308 GGAGCACATTCATTTTCATTGGCAAGATCCAGGGCAGCGCCGCTGGACTTTGGGCTA 1367  
DB 1410 GCCCAAAATACATTTTGAAGAGAGTGGGAAATAGCAGCATAGCCTGTCTCTTGGCTA 1469  
QY 1368 CATGCTGAACCTGACCAACATGATCCCAAGCTTGAGCAACCATTTG 1410  
DB 1470 CATGCTAGCCTGACCAACAGATCCCAAGCTGAAAGCCCTCTG 1512

RESULT 6  
US-09-240-639-3  
; Sequence 3, Application US/09240639  
; Patent No. 6350447  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna-Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
; FILE REFERENCE: 9598-066  
; CURRENT APPLICATION NUMBER: US/09/240.639  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
US-09-240-639-3

Query Match 20.3%; Score 291; DB 3; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 7e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 120 CCAGAACAAAGCATTTGCCAGAAACGTTAACTATGGGATTCGTGGATCGGGTTCCTC 179  
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QY 600 AGTCCCATATGAAACCAATAATCAGGAAACCTTTTGGAGCTTTTGGAGCCTTGGGGAGCCTC 659

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Qy 720 ATTTCGGCTCTATGGCAAGACTACAAATGCTACACACATAGCTTCTTTGGCTATGGAA 779
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Qy 1308 GGAGCACATCCATTTTCAATGGCAAGATCCAGGCGAGCGCGGCTGGACTTTTGGGCTA 1367
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Qy 1368 CATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTG 1410
Db 1471 CATGCTCAGCTGACCAACAGATCCAGCTGAAAGCCCTCTG 1513
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## RESULT 7

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US-09-908-510A-3
; Sequence 3, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischaut, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/361205
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(1669)
; OTHER INFORMATION:
US-09-908-510A-3
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Query Match 20.3%; Score 291; DB 4; Length 2797;
Best Local Similarity 54.3%; Pred. No. 7e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;
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Qy 120 CCAGACAAAGCATTTGCCAGAAACGTTTAAGTATGGATTGCTGGATGCGGTTCTTC 179
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Qy 180 TCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGAGAAATGACACAGGCGTGT 239
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Db 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTGGAAATTTCTGTCTACAGAAATG 1290
QY 1188 GGAGAGATAAAAACATCTTACGTGGAGTAAGGAGAAAGTACCTGAGTGAATACTGCTT 1247
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QY 1248 TTCTGCTACTACATTTCTCTCCCTCTCTCTGCAAGCTATCATTTTTCAGAGCTGATTCCTG 1307
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QY 1308 GGAGCACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGACGCCGCTTGACTTTTGGGCTA 1367
Db 1411 GCCCAAAATACACTTTTGAAGAAAGTGGGGAATAGCAGCATAGCTTGTCTCTTTGGCTA 1470
QY 1368 CATGCTGAACCTGACCAACATGATCCCAAGCTGAGCAACCATTTG 1410
Db 1471 CATGCTCAGCTGACCAACCATGATCCCAAGCTGAAAGCCCTCTG 1513

RESULT 8
US-09-905-744B-3
; Sequence 3, Application US/09905744B
; Patent No. 6780410
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120A
; CURRENT APPLICATION NUMBER: US/09/905,744B
; PRIORITY FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(1669)
; OTHER INFORMATION:
US-09-905-744B-3

Query Match 20.3%; Score 291; DB 4; Length 2797;
Best Local Similarity 54.3%; Pred. No. 7e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 120 CCAGAACAAAGATTGCCAGAAAAGCTTAAAGTATGGGATTTGCTGGATCGGGTTCTTC 179
Db 220 CAAGCAAGAGGTCTCCCTCCAGGACTGAAGTATGGTATGCTGGATGCGGGTCTTC 279
QY 180 TCACACAAAGTTTATACATCTAATAGTGGCGCAGAGAAAGAGATGACAGCGGTGGT 239
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QY 240 GCATCAAGTAGAAGAAATCAGGGTTAAAGGCTCTGGAATCTCAAAATTTGTTTCAGAAAGT 299
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US-10-107-660-3  
; Sequence 3, Application US/10107660  
; Patent No. 6780977  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna-Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS  
; FILE REFERENCE: 9598-066  
; CURRENT APPLICATION NUMBER: US/10/107,660  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: US/09/240,639  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
US-10-107-660-3

Query Match 20.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 7e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 120 CCAGAACAAAGCATCCAGAAAACGTTAAGTAGTGGATTGTGCTGGATCGGGTCTTC 179  
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RESULT 10  
US-10-107-576-3  
; Sequence 3, Application US/10107576  
; Patent No. 6783959  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; TITLE OF INVENTION: ACIDS  
; FILE REFERENCE: 28110/36120H  
; CURRENT APPLICATION NUMBER: US/10/107,576  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-10-107-576-3



		Query Match		20.3%; Score 291; DB 4; Length 2797;			
		Best Local Similarity		54.3%; Pred. No. 7e-86;			
		Matches 707; Conservative		0; Mismatches 575; Indels 21; Gaps 5;			
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Db	220	CAAGCAAGAGTCCCTCCCTCCAGGACTGAAGTATGGTATTGTGCTGGATGCCGGTCTTTC	279				
Qy	180	TCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAATGACACAGGGGTGGT	239				
Db	280	AAGAACCACAGCTACGTGTATCAATGGCCAGAGAAAAAGAGAATAATACCAGGAGTGGT	339				
Qy	240	GCATCAAGTAGAAGATGACAGGGTTAAAGGTCCTGGAACTCTCAAAATTTGTTTCAGAAAGT	299				
Db	340	CAGTCAAAACCTTCAAAATGTAGTGTGAAGGGCTCTGGAATCTCCAGCTATGGAATAAACCC	399				
Qy	300	AAATGAAATAGGCATTTACCTGACTGATTGCATGGAAGAGCTAGGGAAGTCAATCCCAAG	359				
Db	400	CCAAGATGTCCCAGAGCCTTTGAGGAGTGTATGCANNAAGTCAAGGGGCAGGTTCCATC	459				
Qy	360	GTCCAGCACCAAGAGACACCCGTTTACTGGAGCCACGGCAGGATCGCGTTGCTCAG	419				
Db	460	CCACCTCCACGGATCCACCCCAATTCACCTGGGAGCCACGGCTGGGATGCGCTTGTGAG	519				
Qy	420	GATGAAAGTGAAGATTGGCAGACAGGGTTCCTGGATGTGTGGAGAGAGCCTCAGCAA	479				
Db	520	GTGCAAAATGAACAGCAGCTAATGAAGTCTCTGAAAGCATCCAAAGCTACTTCAAGTC	579				
Qy	480	CTACCCCTTTGACTTCCAGGGTCCAGAGTCAATTAATGCGGAAATTTCTGGAGAGAACCTGTGCACATGTG	539				
Db	580	CCAGCCCTTTGACTTTAGGGGTGCTCAATCAATTTCTGGCAAGAAGAGGGGTATATGG	639				
Qy	540	CTGGATTACTATCAACTACTCTCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGTTTCAGCAT	599				
Db	640	ATGGATTACAGCNACTATTTAATGCGAATTTCTCTGGAGAGAACCTGTGCACATGTG	699				
Qy	600	AGTCCCATATGMAACCAATATCAAGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTC	659				
Db	700	GGTGC-----ACCCGCAATGGAGTGGAAACCAACGGGTGCCCTGGACTTAGTGGTGGCTC	753				
Qy	660	TACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCGAGATAATGCTCTGCA	719				
Db	754	CACCCAAATATCTTCTGTGGCAGGAGAGAAGATGGATCTGAACACACGAGCATCATGCA	813				
Qy	720	ATTTGCGCTCTATGGCAAGGACTACAATGTCTTACACACATAGCTTCTTGTGCTATGGAA	779				
Db	814	GGTGTCCCTGTATGCTACGTATACACGCTCTACACACAGCTTCCAGTGTCTATGGCG	873				
Qy	780	GGATCAGGCACTCTGGCAAACTCGGCAAGGACATTCAGGTTTGCAAGTAATGAAA---T	836				
Db	874	GAATGAGGCTGAGAAGAAGTTTCTGGCAATGCTCCTGCAGAAATTCCTCTACCAAAAACCA	933				
Qy	837	TCTCAGGACCCATGCTTTTCACTCCTGGATATAAGNAGGTAGTGAACGTTAAGTGACCTTTA	896				
Db	934	TCTCACCATCCCTGTTTACCCTCGGATTTATAGCATCAGCTTCACCATGGGCCATGTATT	993				
Qy	897	CAAGACCCCTGAC- ----CAAGAGATTTGAGATGACTCTTCCATTCACGACGTTTGA	950				
Db	994	TGATAGCTGTGCACTGTGGACAGAGCCAGAAAGTTATACCCCAATGATGTCATCAC	1053				
Qy	951	AATCAGGGTATTTGAAACTATCAACAATGCCATCAAGCATCTCTGGAGCTTCTTCAACAC	1010				
Db	1054	TTTTGAAGAACTGGGGACCCATCTCTGTGTAAAGGAAGGTGGCTTCCATATTGACTT	1113				
Qy	1011	CAGTTACTGCGCTTACTCCAG- --TGTGCTTCAATGGGATTTTCTTGCCACCACTCCA	1067				
Db	1114	CAAGCTTGGCATGATCAAGAAACCTGTTCTTTTGTATGGGTTTATACGCCAAAGATTA	1173				
Qy	1068	GGGGGATTTGGGGCATTTTCAAGCTTTTACTTTTGTGTGAAGTTTAACTTGACATC	1127				
Db	1174	AGGGCATTTGTGGCTTTTGTGAGGATTTCTACTACACGCCAGTGTCTTTAAATCT---TTC	1230				
Qy	1128	AGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTG	1187				

Db	1231	AGBTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGGAAATTTCTGCTCACAGAAATG	1290				
Qy	1188	GGAGGAGATAAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTTGAGTGAATACTGCTT	1247				
Db	1291	GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGATGAGGTATATGCCGCTCTTACTGCTT	1350				
Qy	1248	TTCTGGTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTCCTG	1307				
Db	1351	CTCAGCCAACTACATCTACCACTTGTGTAACGTTTACAATAATTCACAGAGGAGACTTG	1410				
Qy	1308	GGAGCACATCCATTTTCATTTGGCAAGATCCAGGGCAGCACGCCGCTGGACTTTGGGCTA	1367				
Db	1411	GCCCAAAATACACTTTGAAAAAGAGTGGGAATAGCAGCATAGCCTGGTCTCTTTGGCTA	1470				
Qy	1368	CATGCTGAACCTGACCAACATGATCCAGCTTGAGCAACCATTTG	1410				
Db	1471	CATGCTAGCCTGACCAACCAAGATCCCACTGAAAAGCCCTCTG	1513				

RESULT 11

US-09-905-732B-3

; Sequence 3, Application US/09905732B

; Patent No. 6787328

; GENERAL INFORMATION:

; APPLICANT: Chadwick, Brian Paul

; APPLICANT: Frieschaut, Anna Maria

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND

; FILE REFERENCE: 28110/361208

; CURRENT APPLICATION NUMBER: US/09/905,732B

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: 09/240,639

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 2797

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (83)..(1669)

; OTHER INFORMATION:

US-09-905-732B-3

Query Match 20.3%; Score 291; DB 4; Length 2797;

Best Local Similarity 54.3%; Pred. No. 7e-86;

Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

Qy	120	CCAGAACAAAGCATTCGCCAGAAAAACGTTAAGTATGGGATTGTGCTGGATGCGGGTCTTTC	179				
Db	220	CAAGCAAGAGTCTCCTCCCTCCAGGACTGAAGTATGGTATTGTGCTGGATGCCGGTCTTC	279				
Qy	180	TCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAAATGACACAGCGGTGGT	239				
Db	280	AAGAACCACAGCTACGCTGATCAATGGCCAGCAGAAAAAGAGAAATAATACCGGAGTGGT	339				
Qy	240	GCATCAAGTAGAAGATGACAGGGTTAAAGTTCCTGGAATCTCAAAATTTGTTTCAGAAAGT	299				
Db	340	CAGTCAAAACCTTCAAAATGTAGTGTGAAGGGCTCTGGAATCTCCAGCTATGGAATAAACCC	399				
Qy	300	AAATGAAATAGGCATTTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGAATTCCAAG	359				
Db	400	CCAAGATGTCCCCAGAGCCTTTGAGGAGTGTATGCANNAAGTCAAGGGGCAGGTTCCATC	459				
Qy	360	GTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGGTGTCTCAG	419				
Db	460	CCACCTCCAGGATCCACCCCAATTCACCTGGGAGCCACGGCTGGGATGCGCTTGTGAG	519				
Qy	420	GATGGAAGTGAAGATTGGCAGACAGGGTTCTGGATGTGTGGAGAGGAGCCTCAGCAA	479				
Db	520	GTGCAAAATGAACAGCAGCTAATGAAGTCTTGAAGTCTTGAAGCAATCCAAAGCTACTTCAAGTC	579				



QY 480 CTACCCCTTTGACTCTCAGGGTCCAGGATCAATTACTGGCCAGAGAAAGGCTCTATGG 539  
Db 580 CCAGCCCTTTGACTTTAGGGTCTCAATCAATCAATCTGGCCAGAGAAAGGGTATATGG 639  
QY 540 CTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAACAAAGGTGGTTGAGCAT 599  
Db 640 ATGGATTACAGCCAACTATTAAATGGGAAATTTCTGGAGAGAACTCTGGCACAATGTG 699  
QY 600 AGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTC 659  
Db 700 GGTGC-----ACCGCATGGAGTGAACCCAGGGTGCCTGGACTTAGGTGGTCCCTC 753  
QY 660 TACACAAGTCACTTTTGTACCCCAAAAACAGACTATCGAGTCCCCAGATAATGCTCTGCA 719  
Db 754 CACCCAAATATCCTTCGTGGCAGGAGAGATGATCTGAACACAGCGACATCATGCA 813  
QY 720 ATTTCGCCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGTGCTATGGGAA 779  
Db 814 GGTGTCCCTGTATGGCTACGTATACACAGCTCTACACACAGCTTCCAGTGTCTATGGCG 873  
QY 780 GGATCAGGCACTCTGGCAGAACTGGCCAGGACATTCAGGTTGCAAGTAATGA---T 836  
Db 874 GAATGAGGCTGAGAGAAAGTTTCTGGCAATGCTCTCGCAAAATTTCTTACCAAAACCA 933  
QY 837 TCTCAGGGACCCATGCTTTTTCATCCTCGATATAGAGAGTGTGAACAGTGAAGTCACTTTA 896  
Db 934 TCTCACCATCCCTGTATCCCTCGGATTTATAGCATCAGCTTCAACCATGGCCATGTAAT 993  
QY 897 CAAGACCCCTGAC-----CAAGAGATTTGAGATGACTCTTCCATTCACAGCAGTTGA 950  
Db 994 TGATAGCCTGTGCACTGTGGACAGAGGCTTGAAGGTTTAAAGTGAAGTGTATGCTATC 1053  
QY 951 AATCCAGGTTTGGAACTATCAACATGCTCAAGCATCTCGAGCTCTTCAACAC 1010  
Db 1054 TTTTGAAGGAACTGGGACCCCATCTCTGTGTAGGAGAGGTTCTTGCACCACTCA 1113  
QY 1011 CAGTTACTGCGCTTACTCCAG---TGTGCTTCAATGGGATTTCTTGCACCACTCA 1067  
Db 1114 CAAAGCTTGGCATGATCAAGAACTGTTCTTTTGTATGGGTTTATCAGCCAAAGATTAA 1173  
QY 1068 GGGGGATTGGGGCAATTTTCACTTTTATCTTTGTGATGAAGTATTTTAAACTTGAATC 1127  
Db 1174 AGGCCATTTTGGCTTTTGCAGATTTCTACTACAGCCAGTGTCTTAAATCT---TTC 1230  
QY 1128 AGAGAACTCTCAGGAAAGTGTAGTGAATGAGAAAGTTCTGTGCTCAGCCTTG 1187  
Db 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACTGGAATTTCTGTCTACAGAAATG 1290  
QY 1188 GGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTCAGTGAATPACTGCTT 1247  
Db 1291 GAGTCAGTCCCACTGCTGCTCCCAATTTTGTATGAGGTATATGCCGCTCTTACTGCTT 1350  
QY 1248 TTCTGTGTAOCTAATCT 1307  
Db 1351 CTGAGCCAACTACATCTACCACTTGTGTGTGAACGGTTACAAATTCACAGAGGAGACTTG 1410  
QY 1308 GGAGCACATCCATTTCAATGGCAAGATCAGGGCAGGAGCGCGCTGGACTTTGGGCTA 1367  
Db 1411 GCCCAAAATACATTTGAAAGAAAGTGGGGAATGAGCATAGCTGTGCTCTTGGCTA 1470  
QY 1368 CATGCTGAACCTGACCAATGATCCAGCTGAGCAACCAATG 1410  
Db 1471 CATGCTCAGCTGACCAACAGATCCAGCTGAAGCCCTCTG 1513

RESULT 12  
US-09-923-304-3  
; Sequence 3, Application US/09923304  
; Patent No. 6797471  
; GENERAL INFORMATION:  
; APPLICANT: KATZ, RUTH  
; APPLICANT: JIANG, FENG  
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS

; FILE REFERENCE: UTSC:658US  
; CURRENT APPLICATION NUMBER: US/09/923,304  
; CURRENT FILING DATE: 2001-08-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1672)  
US-09-923-304-3  
  
Query Match 20.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 7e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;  
  
QY 120 CCAGAACAAAGCATTTGCCAGAAACGTTTAAAGTATGGGATTTGTCTGGATGCGGGTTCTTC 179  
Db 220 CAAAGCAAGAGGTCCTCCCTCCAGGACTGAAGTATGGTATTTGCTGGATGCCGGTCTTC 279  
QY 180 TCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAGGAGAAATGACACAGGCGTGT 239  
Db 280 AAGAACCAAGTCTACGTGTATCAATATGGCCAGCAGAAAAAGAGAAATAATACCGGAGTGT 339  
QY 240 GCATCAAGTAGAAGATGCAGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAGT 299  
Db 340 CAGTCAAACTTCAATATGATGTGTAAGGCTCTGGAATCTCCAGTATGGAATTAACCC 399  
QY 300 AAATGAAATAGGCAATTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGAITTCAC 359  
Db 400 CCAAGATGTCCTCCAGAGCCTTTGAGGAGTGTATGCAAAAGTCAAGGGGCGAGTTCCATC 459  
QY 360 GTCCAGCAGCACCAGAGACACCCGTTTACCTGGAGGCGCAGGAGGCAATGCGGTGCTCAG 419  
Db 460 CCACCTCCACGGATCCACCCCAATTCACCTGGAGGCGCAGGCTGGGATGCGCTTGTCTGAG 519  
QY 420 GATGAAAGTGAAGATTTGGCAGACAGGTTCTGATGTGGAGAGAGGCTCAGCAA 479  
Db 520 GTTGCAAAATGAAACAGCAGCTTAATGAAGTCTTGTGAAGCATCCAAAGCTACTTCAAGTC 579  
QY 480 CTACCCCTTTGACTTTCCAGGGTCCAGGATCAATTAATGCGCAAGAGAGGAGTGCCTATGG 539  
Db 580 CCAGCCCTTTGACTTTAGGGTGTCTCAATCAATCAATCTTGGGCAAGAAAGGGGTATATGG 639  
QY 540 CTGGATTACTATCAACTATCTCTCTGGCAGAAATTCAGTCAAGAAACAGAGTGTTCAGCAT 599  
Db 640 ATGGATTACAGCAACTATTTAATGGGAAATTTCTTGGAGAGAAACCTGTGACACATGTG 699  
QY 600 AGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTC 659  
Db 700 GGTGC-----ACCGCATGGAGTGAACCCAGGGTGCCTGGACTTAGGTGGTGGCTTC 753  
QY 660 TACACAAGTCACTTTTGTACCCCAAAAACAGACTATCGAGTCCCCAGATAATGCTCTGCA 719  
Db 754 CACCCAAATATCCTTCGTGGCAGGAGAGATGATCTGAACACAGCGACATCATGCA 813  
QY 720 ATTTCGCCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGTGCTATGGGAA 779  
Db 814 GGTGTCCCTGTATGGCTACGTATACACAGCTCTACACACAGCTTCCAGTGTCTATGGCG 873  
QY 780 GGATCAGGCACTCTGGCAGAACTGGCCAGGACATTCAGGTTGCAAGTAATGA---T 836  
Db 874 GAATGAGGCTGAGAGAAAGTTTCTGGCAATGCTCTCGCAAAATTTCTTACCAAAACCA 933  
QY 837 TCTCAGGGACCCATGCTTTTTCATCCTCGATATAGAGAGTGTGAACAGTGAAGTCACTTTA 896  
Db 934 TCTCACCATCCCTGTATCCCTCGGATTTATAGCATCAGCTTCAACCATGGCCATGTAAT 993  
QY 897 CAAGACCCCTGAC-----CAAGAGATTTGAGATGACTCTTCCATTCACAGCAGTTGA 950  
Db 994 TGATAGCCTGTGCACTGTGGACAGAGGCTTGAAGGTTTAAAGTGAAGTGTATGCTATC 1053

Qy	951	AATCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCCTGGAGCTCTTCAACAC	1010
Db	1054	TTTTGAAGAACTGGGACCCATCTCTGTGTAAAGAGAAGTGGCTTCCCATATTTGACTT	1113
Qy	1011	CAGTTACTGCCCTTACTCCACAG---TGTGCCCTTCAATGGGATTTTCTTGGCCACCACCTCCA	1067
Db	1114	CAAAAGCTTGCCATGATCAAGAAACTGTTCTTTTGTATGGGGTTTATCAGCCAAAGATTAA	1173
Qy	1068	GGGGATTTTTTGGGCAATTTTCAGCTTTTTTACTTTGTGATGAAGTTTTTAAACTTGACATC	1127
Db	1174	AGGGCCATTTTGGCTTTTTCAGGATCTTACTACAGCCAGTGCCTTAAATCT---TTC	1230
Qy	1128	AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCTGTGCTCAGCCTTG	1187
Db	1231	AGGTAGCTTTTCCCTGGACACTTCACTCCAGCACCTCGAAATTTCTGCTCAGAGAAATG	1290
Qy	1188	GGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTT	1247
Db	1291	GAGTCAGCTCCCACTGTGCTCCCAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT	1350
Qy	1248	TTCTGGTACCTACATTTCTCTCCCTCCTTCTGCAAGGCTATCATTTACAGCTGATTCCTG	1307
Db	1351	CTCAGCCAACCTACATCTACCACTTGTGTGTGAACGGTTACAAATTCACAGAGGAGACTTG	1410
Qy	1308	GGAGCACATCCATTTTCATTGGCAAGATCCAGGGCAGCGACCGCGCTGGACTTTGGGCTA	1367
Db	1411	GCCCCAAATACATTTTGAAAAGAAAGTGGGGATAGCAGCATAGCCTGGTCTCTTGGCTA	1470
Qy	1368	CATGCTGAACCTGTACCAACATGATCCAGCTGAGCAACCAATTG	1410
Db	1471	CATGCTCAGCCTGTACCAACACAGATCCCAAGTGTGAAAGCCCTCTG	1513

RESULT 13

```

US-09-949-016-178
; Sequence 178, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-178

```

Query Match	20.3%	Score 291;	DB 4;	Length 2797;
Best Local Similarity	54.3%;	Pred. NO. 7e-86;		
Matches 707;	Conservative	0;	Mismatches 575;	Indels 21; Gaps 5;

Qy	120	CCGAA	CAAAAGCA	TGCGAGAAA	CGTTAAGTATGGGATTCGTGATGCGGGTTC	179
Db	220	CAAGCAAGAGGTCCTCCCTCCAGGACTGAAGTATGGTATTCGTGATGCGGGTTC	279			
Qy	180	TCACACAAGTTTATACATCTATAAGTGCACAGAAAAGAGAGATGCACAGCGGTGT	239			
Db	280	AAGAACCAAGTCATCGTGATCAATGCGCAGAGAAAAGAGATATATCCCGAGGTGT	339			
Qy	240	GCATCAAGTAGAAGAATGCAGGGTTAAGGTCCTGGAAATCTCAAAATTTGTTTCAGAAAGT	299			

340	DB	CAGTCAAACTTCAAATGTAAGTGTGAAGGGCTCTGGAAATCTCCAGACTATGGNAATAACCC	399
300	QY	AAATGAATAAGGCATTTTACCTGACTGATGTGCATGGAAAGACTAGGGAAGTGAATTC	359
400	DB	CCAAGATGCTCCCAAGAGCCTTTTGGAGAGTGATGCAAAAAGTCAAGGGGCAAGTTCCATC	459
360	QY	GTCCAGACACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATGCGGTGCTCAG	419
460	DB	CCACCTCCACGGATCCACCCCAATTCACCTGGAGCCAAGCTGGGATGCGCTTGTCTGAG	519
420	QY	GATGGAAAGTCAAGAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGAGCCTCAGCAA	479
520	DB	GTTGCAAAATGAACACAGAGCTAATGAAGTCTTGTAAAGCATCCAAAGCTACTTCAAGTC	579
480	QY	CTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTA	539
580	DB	CCAGCCCTTTGACTTTAGGGGTGCTCAAATCAATTTCTGGGCAAGAAGGGGTATATGG	639
540	QY	CTGATTTACTATCAACTATCTGTCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGTT	599
640	DB	ATGATTTACAGCCAACTATTTAAATGGGAAATTTCTCTGGAGAAGAAACCTGTGGC	699
600	QY	AGTCCCATATCAAAACCAATATCAGGAAACCTTTTGGAGCTTTTGGACCTTTGGGGAGCCTC	659
700	DB	GGTGC-----ACCGCATGAGTGGGAAACCAAGGTGCTTGGACTT	753
660	QY	TACAAAGTCACTTTTGTACCCCAAAACCAAGTATCGAGTCCCAAGATAATGTCTGCA	719
754	DB	CACCAAAATATCCTTCGTGGCAGAGAGAGATGGAATCTGAAACACAGCGACATCATGCA	813
720	QY	ATTTGGCTCTATGGCAAGGACTAATATGCTACACATAGCTTCTTGTGCTATGGAA	779
814	DB	GGTGTCTCTGTATGGCTACGTATACAGCTCTACACACACAGCTTCAAGTCTATGGCG	873
780	QY	GGATCAGGCACTCTGGCAGAAA	836
874	DB	GAATGGGCTGAGAAGAAGTTTCTGGCAATGCTCCTGCAGAAATTTCTCTACCAAAAACCA	933
837	QY	TCTCAGGGACCCATGCTTTTCACTCTGATATAGAAGTGTAGTGAACGTGAAGTGAACCTTTA	896
934	DB	TCTCACCAATCCCTGTTTACCTCGGATTTATAGCATCAGCTTCAACATGGGCCATGATTT	993
897	QY	CAAGACCCCTGCA-----CAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA	950
994	DB	TGATAGCTGTGCACCTGTGGACACAGGCCAGAAAAGTTATAACCCCAATGATGTCATCAC	1053
951	QY	AATCCAGGTTATGGAAACTATCAACAATGCCATCAAAAGCATCTGGAGCTCTTCAACAC	1010
1054	DB	TTTGAAGGAACTGGGGACCCATCTCTGTGTGAAGGAAAGGTGGCTTCCATATTTTGACTT	1113
1011	QY	CAGTTACTGCTTACTCCCAG--TGTCCTCAATGGGATTTTCTTGCCACCACTCCA	1067
1114	DB	CAAAGCTTGCAATGATCAAGAACTTCTTGTATGGGTTTATCAGCCCAAGATTTAA	1173
1068	QY	GGGGATTTTGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTGCATC	1127
1174	DB	AGGCCATTTTGGCTTTTTCAGGATTTCTACTACAGCCAGTCTTTTAAATCT--TTC	1230
1128	QY	AGAGAAAGTCTCTCAGAAAAGTGACTGATGATGAATAAGTTCTGTGCTCAGCCTTG	1187
1231	DB	AGGTAGCTTTTCCCTGACACCTTTCAACTCCAGCACCTGGAAATTTCTGCTCACAGAAATG	1290
1188	QY	GGAGGAGATAAAACATCTTTACGCTGGAGTTAAAGGAGAACTACCTGAGTGAATACTGCTT	1247
1291	DB	GAGTCAGCTCCCAGCTGCTGCTCCCCAAATTTGATGAGTTATATGCCCGCTCTTACTGCTT	1350
1248	QY	TTCTGTGTACCTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAAGCTGATTCCTG	1307
1351	DB	CTCAGCCAACTACATCTACCACTTGTTTGTGAACGGTTACAAATTCACAGGAGACTTG	1410
1308	QY	GGAGACATCCATTTTCAATGGCAAGATCCAGGGCAGCGACCGCGCTGAGCTTTGGGCTA	1367
1411	DB	GCCTAAATACATTTTGAATAAGAGTGGGAAATAGCAGCATAGCTGCTGCTCTTGGCTA	1470

Qy 1368 CATGCTGAACCTCACCAACATGATCCAGCTGAGCAACCATTTG 1410  
Db 1471 CATGCTAGCCTGACCAACACAGATCCAGCTGAAGCCCTCTG 1513

RESULT 14

US-09-905-743B-3  
; Sequence 3, Application US/09905743B  
; Patent No. 6828423  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; TITLE OF INVENTION: ACIDS  
; FILE REFERENCE: 28110/36120C  
; CURRENT APPLICATION NUMBER: US/09/905,743B  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-09-905-743B-3

Query Match 20.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 7e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;  
Qy 120 CCAGAACAAAGCATTCGCAAGAAACGTTAAGTAGTGGATTGTCTGGATGCGGGTTCTTC 179  
Db 220 CAAGCAAGGTCTCTCCAGACTGAAGTAGTATGTTGCTGGATGCGGGTTCTTC 279  
Qy 180 TCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAGGCGTGT 239  
Db 280 AAGAACACACAGTCTACGTGTATCAATGGCCAGCAGAAAAGAGAAATAATACCGAGTGT 339  
Qy 240 GCATCAAGTAGAAGATGACGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTCAGAAAGT 299  
Db 340 CAGTCAAACTTCAAAATGTAGTGAAGGCTCTGGAATCTCAGCTATGGAATAAACCC 399  
Qy 300 AAATGAAATAGGATTTACCTGACTGATTGATGGAAGAGCTAGGGAAGTGAATCCAAAG 359  
Db 400 CCAAGATGTCCTCCAGAGCCCTTGAGAGGTGTATGCAAAAAGTCAAGGGGAGGTTCATC 459  
Qy 360 GTCCAGACCAAGAGACACCCGTTTACCTGGAGCCACGCGCAGGATCGGTTGCTCAG 419  
Db 460 CCACCTCCAGGATCCACACCCCATTCACCTGGAGCCACGCTGGATGCGCTTGCTGAG 519  
Qy 420 GATGGAAGTGAAGATTGGCAGACAGGTTCTGGATGTGGTGGAGAGAGCCCTCAGCAA 479  
Db 520 GTTGCAAAATGAAACAGCAGCTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC 579  
Qy 480 CTACCCCTTTGACTTCCAGGCTCCAGGATCATTTACTGGCCAAGAGGAGGCTATGG 539  
Db 580 CCAGCCCTTTGACTTTAGGGGTGCTCAATCATTTCTGGCAAGAGAGGGGTATATGG 639  
Qy 540 CTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAAGGTGTTTCAGCAT 599  
Db 640 ATGGATTACAGCAACTATTATTAATGGAAATTTCTGGAGAAACCTGTGGCACAATGT 699  
Qy 600 AGTCCCATATGAACCAACATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTC 659  
Db 700 GGTGC-----ACCCGATGAGTGGAAACCAAGGCTGCGCTTGAAGTGGTGGCT 753  
Qy 660 TACACAAGTCACCTTTTGTATCCCAAAACACAGACTATCGAGTCCCCAGATAATGCTGTGCA 719

Db 754 CACCCAAATATCTCTCGTGGCAGGAGAGATGGATCTGAACACACAGCGCATCATGCA 813  
Qy 720 ATTTGCGCTCTATGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGTATGGGAA 779  
Db 814 GGTGTCCCTGTATGGCTACGTATACACGCTCTACACACACAGCTTCCAGTGTCTATGGCG 873  
Qy 780 GGATCAGGCACCTCTGCGAGAACTGCGCAAGGACATTCAGGTTGCAAGTAATGAAA---T 836  
Db 874 GAATGAGGCTGAGAAGAAGTTTCTGGCAATGCTCTCGAGAAATTCCTTACCAAAACCA 933  
Qy 837 TCTCAGGGACCCATGCTTTTCATCTCGATATAAGAGGTAGTGAAAGTGAAGTGAAGTGA 896  
Db 934 TCTCACCATCTCTGTACCTCGGATTTATAGCATCAGCTTCCACATGGGCCATGTATT 993  
Qy 897 CAAGACCCCTGCAC-----CAAGAGATTTGAGATGACTCTTCCATTCACGACGATTGA 950  
Db 994 TGATAGCCTGTGCACTGTGGACAGAGGCCAGAAAGTTATTAACCCCAATGATGTCAATC 1053  
Qy 951 AATCCAGGCTATTGGAAGTATCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACAC 1010  
Db 1054 TTTTGAAGAACTGGGACCCCATCTCTGTGTAAGAGAGGTGGCTTCCATATTTGACTT 1113  
Qy 1011 CAGTTACTGCCCTTACTCCAG---TGTCCTTCAATGGGATTTTCTTGGCCACCCTCCA 1067  
Db 1114 CAAAGCTTGCCATGATCAAGAAACCTGTTCTTTTGATGGGTTTATCAGSCCAAGATTAA 1173  
Qy 1068 GGGGATTTGGGCACTTTTTCAGCTTTTTCAGCTTTTTCAGTGTGATGAAGTTTAACTTGACATC 1127  
Db 1174 AGGGCCATTTGTGGCTTTTTCAGGATTTCTACTACACAGCAGTGTCTTAAATCT---TTC 1230  
Qy 1128 AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTG 1187  
Db 1231 AGTACTTTTCCCTGGACACCTTCACTCCAGACCTGGAATTTCTGCTCAGAGATTG 1290  
Qy 1188 GGAGGAGATAAAACATCTTACGCTGGAGTAAAGAGAGTACCTGAGTGAATATCTGCTT 1247  
Db 1291 GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT 1350  
Qy 1248 TTCTGGTACTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTCCTG 1307  
Db 1351 CTCAGCCAACTACATCTACCACTTGTGTTGTAACGGTTACAAAATTCACAGAGGAGACTTG 1410  
Qy 1308 GGAGCACATCCATTTTCATTTGGCAAGATCCAGGGCAGCGCGCTGGACTTTTGGGCTA 1367  
Db 1411 GCCCCAATACACTTTGAAAAGAGTGGGGAATAGCAGCATAGCTGTGCTCTCTGGCTA 1470  
Qy 1368 CATGTGAACCTTGACCAACATGATCCAGCTCAGCAACCATTTG 1410  
Db 1471 CATGCTAGCCTGACCAACAGATCCAGCTGAAAAGCCCTCTG 1513

RESULT 15

US-09-949-016-13848  
; Sequence 13848, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13848  
; LENGTH: 46885

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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(46885)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13848

Query Match      18.8%; Score 270.2; DB 4; Length 46885;
Best Local Similarity 98.9%; Pred. No. 5.2e-78;
Matches 272; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      813 CATTGAGGTTGCAAGTAATGAAATCTCAGGACCCATGCTTTTCATCCTGGATATAAGAA 872
Db      26315 CATTGAGGTTGCAAGTAATGAAATCTCAGGACCCATGCTTTTCATCCTGGATATAAGAA 26374

Qy      873 GGTAGTGAACGTAAGTGACCTTTTACAAGACCCCTGCACCAAGAGATTGAGATGACTCT 932
Db      26375 GGTAGTGAACGTAAGTGACCTTTTACAAGACCCCTGCACCAAGAGATTGAGATGACTCT 26434

Qy      933 TCATTCCAGCAGTTTGAATCCAGGGTATTGGAATCTCAACAATGCCATCAAAGCAT 992
Db      26435 TCATTCCAGCAGTTTGAATCCAGGGTATTGGAATCTCAACAATGCCATCAAAGCAT 26494

Qy      993 CCTGAGCTCTTCAACACAGTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTT 1052
Db      26495 CCTGAGCTCTTCAACACAGTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTT 26554

Qy      1053 CTTGCCACCACTCCAGGGGATTTTGGGGCATTTT 1087
Db      26555 CTTGCCACCACTCCAGGGGATTTTGGGGTAAGTT 26589
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Search completed: September 21, 2005, 23:30:35  
Job time : 262.45 secs

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		NAME/KEY: CDS		LOCATION: (1) .. (1434)		US-09-835-147-7	
		Query Match		100.0%; Score 1437; DB 9; Length 1437;			
		Best Local Similarity		100.0%; Pred. No. 0;			
		Matches 1437; Conservative		0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCCCTGTGGATCGACAGGATGCAACTCTCTGTCTTGGATTGCACTAAGTCTTGCACTT	60				
DB	1	ATGGCCCTGTGGATCGACAGGATGCAACTCTCTGTCTTGGATTGCACTAAGTCTTGCACTT	60				
QY	61	GTCAACAAAGTCACACTCTTCAAGTCTTACAAAGAAACACAGACTAACTAGTTCACACC	120				
DB	61	GTCAACAAAGTCACACTCTTCAAGTCTTACAAAGAAACACAGACTAACTAGTTCACACC	120				
QY	121	CAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGTCTGTGATGCGGGTCTTCT	180				
DB	121	CAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGTCTGTGATGCGGGTCTTCT	180				
QY	181	CACAAAGTTTATACATCTATAGTGGCCAGCAAGAAAGAGAAATGACACAGCGTGGTG	240				
DB	181	CACAAAGTTTATACATCTATAGTGGCCAGCAAGAAAGAGAAATGACACAGCGTGGTG	240				
QY	241	CATCAAGTAGAAGATGCGGGTTAAAGTCTTGGAAATCTCAAAATTTTGTTCAGAAAGTA	300				
DB	241	CATCAAGTAGAAGATGCGGGTTAAAGTCTTGGAAATCTCAAAATTTTGTTCAGAAAGTA	300				
QY	301	AATGAAATAGGCATTTACCTGACTGATTGATGCAAGAAAGAGCTAGGGAAGTGAATCCAAAG	360				
DB	301	AATGAAATAGGCATTTACCTGACTGATTGATGCAAGAAAGAGCTAGGGAAGTGAATCCAAAG	360				
QY	361	TCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGCGAGGATGCGGTGCTCAGG	420				
DB	361	TCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGCGAGGATGCGGTGCTCAGG	420				
QY	421	ATGGAAGTGAAGATTTGGCAGACAGGTTCTGGATGTGTGGAGAGGAGCCTCAGCAAC	480				
DB	421	ATGGAAGTGAAGATTTGGCAGACAGGTTCTGGATGTGTGGAGAGGAGCCTCAGCAAC	480				
QY	481	TACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTTGGCCAAAGGAAGTGTCTATGGC	540				
DB	481	TACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTTGGCCAAAGGAAGTGTCTATGGC	540				
QY	541	TGATTTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAACAAGTGGTTTACGATA	600				
DB	541	TGATTTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAACAAGTGGTTTACGATA	600				
QY	601	GTCCCATATGAAACCAATATACAGAAACCTTTGGAGCTTTGGACCTTGGGGAGCCTCT	660				
DB	601	GTCCCATATGAAACCAATATACAGAAACCTTTGGAGCTTTGGACCTTGGGGAGCCTCT	660				
QY	661	ACAAAGTCACTTTTGTACCCCAAAACCCAGACTATCGAGTCCCCAGATAATGCTCTGCAA	720				
DB	661	ACAAAGTCACTTTTGTACCCCAAAACCCAGACTATCGAGTCCCCAGATAATGCTCTGCAA	720				
QY	721	TTTGGCTCTATGGCAAGACTACAATGTCTACACATAGCTTCTTGTGCTATGGGAAG	780				
DB	721	TTTGGCTCTATGGCAAGACTACAATGTCTACACATAGCTTCTTGTGCTATGGGAAG	780				
QY	781	GATCAGGCACTCTGGCAGAACTGGCCAGGACATTGAGTTCGAAGTAAATTTCTC	840				
DB	781	GATCAGGCACTCTGGCAGAACTGGCCAGGACATTGAGTTCGAAGTAAATTTCTC	840				
QY	841	AGGAGCCCATGCTTTTCACTCTGGATATAAGAAAGTAGTGAACCTTGAAGTTCACAG	900				
DB	841	AGGAGCCCATGCTTTTCACTCTGGATATAAGAAAGTAGTGAACCTTGAAGTTCACAG	900				
QY	901	ACCCCTGCAACCAAGAGATTGATGACTCTTCCATTCAGCAGTTTGAATCCAGGTT	960				
DB	901	ACCCCTGCAACCAAGAGATTGATGACTCTTCCATTCAGCAGTTTGAATCCAGGTT	960				
QY	961	ATTGGAAACTATCAACAAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCACTTACTGC	1020				

RESULT 2

US-09-835-147-25  
; Sequence 25, Application US/09835147  
; Patent No. US2002002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimbel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 1464  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) .. (1461)  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
; OTHER INFORMATION: construct of human CD39  
US-09-835-147-25

Query Match		97.4%; Score 1400; DB 9; Length 1464;	
Best Local Similarity		98.2%; Pred. No. 0;	
Matches 1437; Conservative		0; Mismatches 0; Indels 27; Gaps 1;	
QY	1	ATGGCCCTGTGGATCGACAGGATGCAACTCTCTGTCTTGGCAATGCACTAAGTCTTGCACTT	60
DB	1	ATGGCCCTGTGGATCGACAGGATGCAACTCTCTGTCTTGGCAATGCACTAAGTCTTGCACTT	60



QY 61 GTCACAAACAGTGCACCTACTTCAAGTTCTACAAAGAAAAACACAGCTAACTAGTTC---- 116  
Db 61 GTCACAAACAGTGCACCTACTTCAAGTTCTACAAAGAAAAACACAGCTAACTAGTTCAGGA 120  
QY 117 -----NACCCAGAACNAAGCATTTGCCAGNAACCCCTTAAGTAT 153  
Db 121 GACTCAAAAGATGACGATGACAAAACCCAGAACAAAGCATTTGCCAGNAACCCCTTAAGTAT 180  
QY 154 GGGATTGTCTGGATGCGGGTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCA 213  
Db 181 GGGATTGTCTGGATGCGGGTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCA 240  
QY 214 GAAAGGGAATGACACAGCGGTGTGTCATCAAGTAGAAGATGACAGGGTTAAAGTCT 273  
Db 241 GAAAGGGAATGACACAGCGGTGTGTCATCAAGTAGAAGATGACAGGGTTAAAGTCT 300  
QY 274 GGAATCTCAAAATTTGTCAGAAAGTAAATGAATAGGCATTTACTGATGATTCGATG 333  
Db 301 GGAATCTCAAAATTTGTCAGAAAGTAAATGAATAGGCATTTACTGATGATTCGATG 360  
QY 334 GAAAGAGCTAGGGAAGTGAATCCAAAGTCCAGCACCAAGACACCCGGTTTACCTGGGA 393  
Db 361 GAAAGAGCTAGGGAAGTGAATCCAAAGTCCAGCACCAAGACACCCGGTTTACCTGGGA 420  
QY 394 GCCACGGCAGGATGCGGTGTCAGGATGGAAGTGAAGATGGCAGACAGGGTTCTG 453  
Db 421 GCCACGGCAGGATGCGGTGTCAGGATGGAAGTGAAGATGGCAGACAGGGTTCTG 480  
QY 454 GATGTGTGGAGAGAGCTCAGCAACTACCCCTTTGACTCCAGGGTGCAGGATCAT 513  
Db 481 GATGTGTGGAGAGAGCTCAGCAACTACCCCTTTGACTCCAGGGTGCAGGATCAT 540  
QY 514 ACTGCCCAAGAGAGGTGCTTATGCTGATTTACTCAACTATCTGCTGGCAAAATTC 573  
Db 541 ACTGCCCAAGAGAGGTGCTTATGCTGATTTACTCAACTATCTGCTGGCAAAATTC 600  
QY 574 AGTCAGAAAACAGGTGTTACGATAGTCCCATATGAACCAATTAATCAGGAAACCTTT 633  
Db 601 AGTCAGAAAACAGGTGTTACGATAGTCCCATATGAACCAATTAATCAGGAAACCTTT 660  
QY 634 GGAGCTTTGGACCTTTGGGGAGCCCTACACAGTCACTTTTGTACCCCAAAACAGACT 693  
Db 661 GGAGCTTTGGACCTTTGGGGAGCCCTACACAGTCACTTTTGTACCCCAAAACAGACT 720  
QY 694 ATCGAGTCCCAAGATAATGCTCTGCAATTTGSCCTCTATGGCAAGSACTACAGTCTAC 753  
Db 721 ATCGAGTCCCAAGATAATGCTCTGCAATTTGSCCTCTATGGCAAGSACTACAGTCTAC 780  
QY 754 ACACATAGCTTCTTGTCTATGGGAAGGATCAGGCACCTTGCCAGAAAACCTGGCCAAAGAC 813  
Db 781 ACACATAGCTTCTTGTCTATGGGAAGGATCAGGCACCTTGCCAGAAAACCTGGCCAAAGAC 840  
QY 814 ATTGAGTTGCAAGTAATGAATTTCTCAGGGACCCATGTTTCACTCCCTGGATATAAGAG 873  
Db 841 ATTGAGTTGCAAGTAATGAATTTCTCAGGGACCCATGTTTCACTCCCTGGATATAAGAG 900  
QY 874 GTAGTGAACGTAAGTGACCTTTTACAAAGACCCCTGCACCAAGAGATTTGAGATGACTCT 933  
Db 901 GTAGTGAACGTAAGTGACCTTTTACAAAGACCCCTGCACCAAGAGATTTGAGATGACTCT 960  
QY 934 CCATTTCCAGCAGTTTGAATCCAGGGTATTTGAAACTATCAACATGATCCATCAAGCATC 993  
Db 961 CCATTTCCAGCAGTTTGAATCCAGGGTATTTGAAACTATCAACATGATCCATCAAGCATC 1020  
QY 994 CTGGAGCTCTTCAACACAGTTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTTC 1053  
Db 1021 CTGGAGCTCTTCAACACAGTTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTTC 1080  
QY 1054 TTGCCACACATCCAGGGGATTTTGGGCATTTTTCAGCTTTTACTTTTGTGATGAGTTT 1113  
Db 1081 TTGCCACACATCCAGGGGATTTTGGGCATTTTTCAGCTTTTACTTTTGTGATGAGTTT 1140

QY 1114 TTAAACTTGACATCAGAGAAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTC 1173  
Db 1141 TTAAACTTGACATCAGAGAAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTC 1200  
QY 1174 TGTGCTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTG 1233  
Db 1201 TGTGCTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTG 1260  
QY 1234 AGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTCCTTCTGCAAGGCTATCATTTTC 1293  
Db 1261 AGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTCCTTCTGCAAGGCTATCATTTTC 1320  
QY 1294 ACAGCTGATTTCTGGGAGCACATTCATTTTCTATGCAAGATCCAGGGGAGCGACGCCGC 1353  
Db 1321 ACAGCTGATTTCTGGGAGCACATTCATTTTCTATGCAAGATCCAGGGGAGCGACGCCGC 1380  
QY 1354 TGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCC 1413  
Db 1381 TGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCC 1440  
QY 1414 ACACCTCTCTCCCACTCCACCTAA 1437  
Db 1441 ACACCTCTCTCCCACTCCACCTAA 1464

RESULT 3

US-09-835-147-5  
; Sequence 5, Application US/09835147  
; Patent No. US2002002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
; OTHER INFORMATION: construct of human CD39  
; NAME/KEY: CDS  
; LOCATION: (1)..(1362)  
US-09-835-147-5

Query Match 95.0%; Score 1365; DB 9; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 GCACCTACTTCAAGTTCTACAAAGAAAACACAGCTAACTAGTTTCAACCCAGAACAAAGCA 132  
Db 1 GCACCTACTTCAAGTTCTACAAAGAAAACACAGCTAACTAGTTTCAACCCAGAACAAAGCA 60  
QY 133 TTGCAGAAAACGTTAAGTATGGGATTTGTGCTGATGCGGGTTCTTCTCACACAAGTTTA 192  
Db 61 TTGCAGAAAACGTTAAGTATGGGATTTGTGCTGATGCGGGTTCTTCTCACACAAGTTTA 120  
QY 193 TACATCTATAGTGGCCAGCAGAAAAGAGAAATCACACAGCGGTGTCATCAAGTAGAA 252

Db 121 TACATCTATAAGTGGCCAGCAGAGAAAGGAGAAATGACACAGGCGTGGTGATCAAGTAGAA 180  
Qy 253 GAATGACGGGTTAAAGTCTCGAATCTCAAAATTTGTTTCAGAAAAGTAATGAATAGGC 312  
Db 181 GAATGACGGGTTAAAGTCTCGAATCTCAAAATTTGTTTCAGAAAAGTAATGAATAGGC 240  
Qy 313 ATTTACTGACTGATTTGCTAGGAAAGAGCTPAGGAAAGTGAATCCAAAGGTCCACAGCCAA 372  
Db 241 ATTTACTGACTGATTTGCTAGGAAAGAGCTPAGGAAAGTGAATCCAAAGGTCCACAGCCAA 300  
Qy 373 GAGACACCCCTTTACCTGGGAGCCACGGCAGGATCGGTTGCTCAGGATGGAAAGTGAA 432  
Db 301 GAGACACCCGTTTACCTGGGAGCCACGGCAGGATCGGTTGCTCAGGATGGAAAGTGAA 360  
Qy 433 GAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCCTAGCAACTACCCCTTTGAC 492  
Db 361 GAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCCTAGCAACTACCCCTTTGAC 420  
Qy 493 TTCCAGGGTCCAGGATCATTTACTGSCCAAGAGAGGTCCTTATGGCTGGATTACTATC 552  
Db 421 TTCCAGGGTCCAGGATCATTTACTGSCCAAGAGAGGTCCTTATGGCTGGATTACTATC 480  
Qy 553 AACTATCTGCTGGGCAAAATTCAGTCAGAAAAAAGGTGGTTTCAGCATAGTCCCATATGAA 612  
Db 481 AACTATCTGCTGGGCAAAATTCAGTCAGAAAAAAGGTGGTTTCAGCATAGTCCCATATGAA 540  
Qy 613 ACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTTGGGGAGGCTCTACACAAGTCACT 672  
Db 541 ACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTTGGGGAGGCTCTACACAAGTCACT 600  
Qy 673 TTTGTATCCCAAAACAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTTGGCCCTTAT 732  
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Qy 733 GGCAAGGACTACAAATGTCTACACATAGTCTTCTGTGCTATGGGAAGGATCAGGCACTC 792  
Db 661 GGCAAGGACTACAAATGTCTACACATAGTCTTCTGTGCTATGGGAAGGATCAGGCACTC 720  
Qy 793 TGGCAGAACTGGCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGAGCCATGC 852  
Db 721 TGGCAGAACTGGCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGAGCCATGC 780  
Qy 853 TTTTCATCTCGATATAGAAGGTAGTGAAGTAAAGTACCTTTTACAGACCCCTCGACC 912  
Db 781 TTTTCATCTCGATATAGAAGGTAGTGAAGTAAAGTACCTTTTACAGACCCCTCGACC 840  
Qy 913 AAGAGATTTGAGATGACTCTTCCATTCACAGCTTTGAAATCCAGGGTATTTGGAACATAT 972  
Db 841 AAGAGATTTGAGATGACTCTTCCATTCACAGCTTTGAAATCCAGGGTATTTGGAACATAT 900  
Qy 973 CAACAATGCCATCAAGGATCTGGAGCTCTTCAACACAGTATCTGCCCTTACTCCAG 1032  
Db 901 CAACAATGCCATCAAGGATCTGGAGCTCTTCAACACAGTATCTGCCCTTACTCCAG 960  
Qy 1033 TGTGCCCTTCAATGGGATTTCTTGGCCACCACTCCAGGGGATTTTGGGGATTTTTCAGCT 1092  
Db 961 TGTGCCCTTCAATGGGATTTCTTGGCCACCACTCCAGGGGATTTTGGGGATTTTTCAGCT 1020  
Qy 1093 TTTTACTTTTGTGATGAAGTTTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1152  
Db 1021 TTTTACTTTTGTGATGAAGTTTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1080  
Qy 1153 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCTTTGGAGAGAGATATAAATCATCTTAGCT 1212  
Db 1081 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCTTTGGAGAGAGATATAAATCATCTTAGCT 1140  
Qy 1213 GGAGTAAAGAGAGAGTACCTGAGTGAATCTGCTTTTCTGGTACCTACATTTCTCCCTC 1272  
Db 1141 GGAGTAAAGAGAGAGTACCTGAGTGAATCTGCTTTTCTGGTACCTACATTTCTCCCTC 1200  
Qy 1273 CTTCGCAAGGCTATCATTTTACAGCTGATTTCTCGGAGACACATCCATTTTCAATTTGCAAG 1332  
Db 1201 CTTCGCAAGGCTATCATTTTACAGCTGATTTCTCGGAGACACATCCATTTTCAATTTGCAAG 1260

Qy 1333 ATCCAGGGCAGGACGCGGCTGGACTTTTGGCTACATGCTGAACCTGACCAACATGATC 1392  
Db 1261 ATCCAGGGCAGGACGCGGCTGGACTTTTGGCTACATGCTGAACCTGACCAACATGATC 1320  
Qy 1393 CCAGCTGAGCAACCACTTTGTCCACACACTCTCTCCCACTCCACCTAA 1437  
Db 1321 CCAGCTGAGCAACCACTTTGTCCACACACTCTCTCCCACTCCACCTAA 1365

## RESULT 4

US-09-835-147-1  
; Sequence 1, Application US/09835147  
; Patent No. US2002002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(1596)  
US-09-835-147-1

Query Match 91.8%; Score 1319.2; DB 9; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 113 GTTCAACCCAGAACAAAGCAATTCGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATGCGG 172  
Db 173 GGTTCACCCAGAACAAAGCAATTCGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATGCGG 232  
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGAGAAAAGGAGAGATGACACAG 232  
Db 233 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGAGAAAAGGAGAGATGACACAG 292  
Qy 233 GGTGGTGCATCAAGTAGAAGAAATCAGGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292  
Db 293 GGTGGTGCATCAAGTAGAAGAAATCAGGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 352  
Qy 293 AGAAAGTAAATGAAATPAGGCATTTTACCTGATTCATGTAATGGAAGAGCTAGGGAAGTGA 352  
Db 353 AGAAAGTAAATGAAATPAGGCATTTTACCTGATTCATGTAATGGAAGAGCTAGGGAAGTGA 412  
Qy 353 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACTCTGGGAGCCACGGCAGGCATCGGT 412  
Db 413 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACTCTGGAGCCACGGCAGGCATCGGT 472  
Qy 413 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGGGTTCTTGGATGTGGTGGAGAGGAGCC 472  
Db 473 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGGGTTCTTGGATGTGGTGGAGAGGAGCC 532  
Qy 473 TCAGCAACTACCCCTTTGACTTTCCAGGGTGCAGGATCATTTACTGGCCCAAGAGAGGTTG 532  
Db 533 TCAGCAACTACCCCTTTGACTTTCCAGGGTGCAGGATCATTTACTGGCCCAAGAGAGGTTG 592

QY 533 CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 592  
Db CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 652  
QY 593 TCAGCATAGTCCCATATGAAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 652  
Db 653 TCAGCATAGTCCCATATGAAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 712  
QY 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGAGTATCCAGTCCCAAGATAATG 712  
Db 713 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGAGTATCCAGTCCCAAGATAATG 772  
QY 713 CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTTCTTGCT 772  
Db 773 CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTTCTTGCT 832  
QY 773 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTCGCAAGTAATG 832  
Db 833 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTCGCAAGTAATG 892  
QY 833 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAAAGTAGTGAACGTAAAGTGACC 892  
Db 893 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAAAGTAGTGAACGTAAAGTGACC 952  
QY 893 TTTTCAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAA 1012  
Db 953 TTTTCAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAA 1012  
QY 953 TCCAGGATTTGGAACTATCAACATGCCATCAAGCATCTGGAGCTCTTCAACACCA 1012  
Db 1013 TCCAGGATTTGGAACTATCAACATGCCATCAAGCATCTGGAGCTCTTCAACACCA 1072  
QY 1013 GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCACCCTCTCAGGGGG 1072  
Db 1073 GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCACCCTCTCAGGGGG 1132  
QY 1073 ATTTTGGGGCAATTTTCACTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1132  
Db 1133 ATTTTGGGGCAATTTTCACTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1192  
QY 1133 AAGTCTCTCAGGAAGGTGACTGAGATGATGAAGTTTCTTGGCACCCTCTCAGGGGG 1192  
Db 1193 AAGTCTCTCAGGAAGGTGACTGAGATGATGAAGTTTCTTGGCACCCTCTCAGGGGG 1252  
QY 1193 AGATAAAACATCTTACCTGAGTAAAGGAGAGTACCTCAGTGAATACTGCTTTTCTG 1252  
Db 1253 AGATAAAACATCTTACCTGAGTAAAGGAGAGTACCTCAGTGAATACTGCTTTTCTG 1312  
QY 1253 GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCAATTTCAAGCTGATTTCTTGGAGC 1312  
Db 1313 GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCAATTTCAAGCTGATTTCTTGGAGC 1372  
QY 1313 ACATCCATTTCAATGGGCAAGATCCAGGCACGACCGCGCTGGAGCTTTGGGCTACATGC 1372  
Db 1373 ACATCCATTTCAATGGGCAAGATCCAGGCACGACCGCGCTGGAGCTTTGGGCTACATGC 1432  
QY 1373 TGAACCTTGACCAACATGATCCAGCTGAGCAACATTTGTCCACACCTCTCTCCCACTCCA 1432  
Db 1433 TGAACCTTGACCAACATGATCCAGCTGAGCAACATTTGTCCACACCTCTCTCCCACTCCA 1492  
QY 1433 CCTA 1436  
Db 1493 CCTA 1496

RESULT 5

US-10-646-308-29  
; Sequence 29, Application US/10646308  
; Publication No. US20040136992A1  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, Paul B. J.  
; APPLICANT: DEISHER, Theresa A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE  
; FILE REFERENCE: 3432-B  
; CURRENT APPLICATION NUMBER: US/10/646,308  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: --to be assigned--  
; PRIOR FILING DATE: 2003-08-12  
; PRIOR APPLICATION NUMBER: 60/406,418  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 1599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(1596)  
US-10-646-308-29

Query Match 91.8%; Score 1319.2; DB 19; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAAACAAAGCATTTGCCAGAAACGTTAAGTATGGGATTTGCTGGATGGG 172  
Db 173 GGTTCAGCCAGAACAAAGCATTTGCCAGAAACGTTAAGTATGGGATTTGCTGGATGGG 232  
QY 173 GTTCTCTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAGAGAGATGACACAG 232  
Db 233 GTTCTCTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAGAGAGATGACACAG 292  
QY 233 GCGTGGTGCATCAAGTAGAAGATTCAGGGTTAAAGGTCCTTGGAACTCTCAAAATTTGTTTC 292  
Db 293 GCGTGGTGCATCAAGTAGAAGATTCAGGGTTAAAGGTCCTTGGAACTCTCAAAATTTGTTTC 352  
QY 293 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGGAAAGAGCTAGGGAAGTGA 352  
Db 353 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGGAAAGAGCTAGGGAAGTGA 412  
QY 353 TTCCAAGGTCCACACACCAAGAGACACCGTTTACCTGGGAGCCACGCGCATGCGGT 412  
Db 413 TTCCAAGGTCCACACACCAAGAGACACCGTTTACCTGGGAGCCACGCGCATGCGGT 472  
QY 413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGGCC 472  
Db 473 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGGCC 532  
QY 473 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCAAAGAGGTG 532  
Db 533 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCAAAGAGGTG 592  
QY 533 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 592  
Db 593 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 652  
QY 593 TCAGCATAGTCCCATATGAAACCAATTAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 652  
Db 653 TCAGCATAGTCCCATATGAAACCAATTAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 712  
QY 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGAGTATCGAGTCCCAAGATAATG 712  
Db 713 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGAGTATCGAGTCCCAAGATAATG 772  
QY 713 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGCT 772  
Db 773 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGCT 832  
QY 773 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832  
Db 833 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 892  
QY 833 AAATTTCTCAGGACCCCATGCTTTTCATCTGGATATAAGAAAGTAGTGAACGTAAAGTGACC 892

893 AAATTCTCAGGACCACCATGTTTCATCTCTGGATATAGAAGGTAGTGAACGTAAGTGACC 952  
893 TTTCAGAGACCCCTGCACCAAGAGATTTTGAGATGACTCTTCCATTCACGAGTTTGAA 952  
953 TTTCAGAGACCCCTGCACCAAGAGATTTTGAGATGACTCTTCCATTCACGAGTTTGAA 1012  
953 TCAGGGTATTTGAAACTATCAACAATGCATCAAAAGCATCTGGAGCTCTTCAACACCA 1012  
1013 TCAGGGTATTTGAAACTATCAACAATGCATCAAAAGCATCTGGAGCTCTTCAACACCA 1072  
1013 GTTACTGCCCTTACTCCCGAGTGTCCCTCAATGGGATTTTCTTGCCACACTCCAGGGG 1072  
1073 GTTACTGCCCTTACTCCCGAGTGTCCCTCAATGGGATTTTCTTGCCACACTCCAGGGG 1132  
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1193 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCGCTTGGGAGG 1252  
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1253 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTCTG 1312  
1253 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGC 1312  
1313 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGC 1372  
1313 ACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGGCTTGGGCTACATGC 1372  
1373 ACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGGCTTGGGCTACATGC 1432  
1373 TGAACCTGACCAACATGATCCCAAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1432  
1433 TGAACCTGACCAACATGATCCCAAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1492  
1433 CCTA 1436  
1493 CCTA 1496

RESULT 6

US-10-641-643-1475  
; Sequence 1475, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Jeffrey J. Seilhamer  
; Susan G. Stuart  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1475:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g765255  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1475 :  
US-10-641-643-1475  
  
Query Match 91.8%; Score 1319.2; DB 18; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAACGTTTAAGTATGGGATTTGTCTGGATCGCG 172  
Db 174 GGTTCACCCAGAACAAAGCATTTGCCAGAAACGTTTAAGTATGGGATTTGTCTGGATCGCG 233  
  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAGGAGATGACACAG 232  
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAGGAGATGACACAG 293  
  
QY 233 GGTGCGTGCATCAAGTAGAAGTAAGTACAGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292  
Db 294 GGTGCGTGCATCAAGTAGAAGTAAGTACAGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
  
QY 293 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGAGCTAGGGAAGTGA 352  
Db 354 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGAGCTAGGGAAGTGA 413  
  
QY 353 TTCCAAGGTCCAGCACCAAGAGAGACACCGTTTACTGGAGCCACGGCAGCATCGCGT 412  
Db 414 TTCCAAGGTCCAGCACCAAGAGAGACACCGTTTACTGGAGCCACGGCAGCATCGCGT 473  
  
QY 413 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGCGGTTCTGGATGTGGTGAGAGAGCC 472  
Db 474 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGCGGTTCTGGATGTGGTGAGAGAGCC 533  
  
QY 473 TCAGCAACTACCCCTTTGACTTTCCAGGTTGCCAGGATCAATTAAGTCCCAAGAGGAGGTTG 532  
Db 534 TCAGCAACTACCCCTTTGACTTTCCAGGTTGCCAGGATCAATTAAGTCCCAAGAGGAGGTTG 593  
  
QY 533 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGTGGT 592  
Db 594 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGTGGT 653  
  
QY 593 TCAGCATAGTCCCATATGAACCAATAATCAAGAAAACCTTTGGAGCTTTGGACCTTGGGG 652  
Db 654 TCAGCATAGTCCCATATGAACCAATAATCAAGAAAACCTTTGGAGCTTTGGACCTTGGGG 713  
  
QY 653 GAGCCTCTACACAAGTCACTTTTGTATCCCAAAAACAGACTATTCAGTCCCAAGATAATG 712  
Db 714 GAGCCTCTACACAAGTCACTTTTGTATCCCAAAAACAGACTATTCAGTCCCAAGATAATG 773  
  
QY 713 CTCCTCAATTTGCGCTCTATGCAAGGACTCAATGTCTTACACATAGCTTCTTGTGCT 772  
Db 774 CTCCTCAATTTGCGCTCTATGCAAGGACTCAATGTCTTACACATAGCTTCTTGTGCT 833  
  
QY 773 ATGGGAAGGATCAGGCACCTCTGCGCAAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832  
Db 834 ATGGGAAGGATCAGGCACCTCTGCGCAAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893  
  
QY 833 AAATTTCTCAGGACCCCATGCTTTTCATCTCTGGATATATAAGAGGTAGTGAACGTAAGTGACC 892  
|||||

Db 894 AAATTCTCAGGACCCATCGCTTTTCATCTCGGATATGAAGGTAGTGAACGTAAAGTGACC 953  
Qy 893 TTTTACAAGACCCCTGCAACAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 952  
Db 954 TTTTACAAGACCCCTGCAACAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 1013  
Qy 953 TCCAGGATTTGGAACATATCAACATGCGCATCAAGCATCTGGAGCTCTTCAACACCA 1012  
Db 1014 TCCAGGATTTGGAACATATCAACATGCGCATCAAGCATCTGGAGCTCTTCAACACCA 1073  
Qy 1013 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCCACCCTCCAGGGGG 1072  
Db 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCCACCCTCCAGGGGG 1133  
Qy 1073 ATTTGGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1132  
Db 1134 ATTTTGGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1193  
Qy 1133 AGTCTCTCAGGAAAAGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCCTGGGAGG 1192  
Db 1194 AGTCTCTCAGGAAAAGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCCTGGGAGG 1253  
Qy 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1252  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1313  
Qy 1253 GTACCTACATCTCTCCCTCTCTTCTGCAAGGCTATCATTTACACGCTGATTTCTCGGAGC 1312  
Db 1314 GTACCTACATCTCTCCCTCTCTTCTGCAAGGCTATCATTTACACGCTGATTTCTCGGAGC 1373  
Qy 1313 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGC 1372  
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGC 1433  
Qy 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTCCACACCTCTTCCCACTCCA 1432  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTTCCCACTCCA 1493  
Qy 1433 CCTA 1436  
Db 1494 CCTA 1497

RESULT 7

US-10-934-998-290  
; Sequence 290. Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; PRIORITY FILING DATE: 2004-09-03  
; PRIORITY FILING DATE: 2003-03-04  
; PRIORITY FILING DATE: 2003-03-04  
; PRIORITY FILING DATE: 2002-03-04  
; PRIORITY FILING DATE: 2002-03-04  
; PRIORITY FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 290  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Genbank/S73813  
; DATABASE ENTRY DATE: 1995-04-12  
US-10-934-998-290

Query Match 91.8%; Score 1319.2; DB 22; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 113 GTTCAACCCAGAACAAACGATTTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGCGG 172  
Db 174 GTTCAACCCAGAACAAACGATTTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGCGG 233  
Qy 173 GTTCTCTCTCACCAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAGAGAGATGACACAG 232  
Db 234 GTTCTCTCTCACCAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAGAGAGATGACACAG 293  
Qy 233 GCGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTTC 292  
Db 294 GCGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTTC 353  
Qy 293 AGAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 352  
Db 354 AGAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 413  
Qy 353 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 412  
Db 414 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 473  
Qy 413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 472  
Db 474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 533  
Qy 473 TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCATTTACTGGCCCAAGGAGAGTG 532  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCATTTACTGGCCCAAGGAGAGTG 593  
Qy 533 CCTATGGCTGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 592  
Db 594 CCTATGGCTGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 653  
Qy 593 TCAGCATAGTCCCATATGAAAACCAATATCAGGAAAACCTTTGGAGCTTTGACCTTGGGG 652  
Db 654 TCAGCATAGTCCCATATGAAAACCAATATCAGGAAAACCTTTGGAGCTTTGACCTTGGGG 713  
Qy 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAAGTAATG 712  
Db 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAAGTAATG 773  
Qy 713 CTCTGCAATTTTCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGCTGT 772  
Db 774 CTCTGCAATTTTCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGCTGT 833  
Qy 773 ATGGGAAGGATCAGGCACTCTGGCAGAAAACCTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832  
Db 834 ATGGGAAGGATCAGGCACTCTGGCAGAAAACCTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893  
Qy 833 AAATTTCTCAGGACCCCATGCTTTTCATCTGGATATAGAAGGTAGTGAACGTAAAGTACC 892  
Db 894 AAATTTCTCAGGACCCCATGCTTTTCATCTGGATATAGAAGGTAGTGAACGTAAAGTACC 953  
Qy 893 TTTTACAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGATTTGAAA 952  
Db 954 TTTTACAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGATTTGAAA 1013  
Qy 953 TCCAGGATTTGGAACCTATCAACAAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCA 1012  
Db 1014 TCCAGGATTTGGAACCTATCAACAAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCA 1073  
Qy 1013 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCCTCCAGGGGG 1072  
Db 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCCTCCAGGGGG 1133  
Qy 1073 ATTTTGGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1132  
Db 1134 ATTTTGGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1193  
Qy 1133 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGG 1192

Db	1194	AGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTCTCAGCCTTGGGAGG	1253
Qy	1193	AGATAAAAACATCTTACGCTGGAGTAAAGAGAAAGTAACTGAGTGAATACTGCTTTTCTG	1252
Db	1254	AGATAAAAACATCTTACGCTGGAGTAAAGAGAAAGTAACTGAGTGAATACTGCTTTTCTG	1313
Qy	1253	GTACCTACATCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTCCTGGGAGC	1312
Db	1314	GTACCTACATCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTCCTGGGAGC	1373
Qy	1313	ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACGCCGCTGGACTTTGGGCTACATGC	1372
Db	1374	ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACGCCGCTGGACTTTGGGCTACATGC	1433
Qy	1373	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA	1432
Db	1434	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA	1493
Qy	1433	CCTA 1436	
Db	1494	CCTA 1497	

RESULT 8

US-10-934-998-46  
; Sequence 46, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; FILE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF  
; TITLE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: Patencin version 3.2  
; SEQ ID NO 46  
; LENGTH: 2081  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: GS-N45  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GENBANK/AJ131313  
; DATABASE ENTRY DATE: 2000-01-19  
; RELEVANT RESIDUES: (1)..(2081)  
US-10-934-998-46

Query Match 91.8%; Score 1319.2; DB 22; Length 2081;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	113	GTTCAACCCAGACAAGCAATGCCAGAAAACGTTAAGTATGGATTGCTGGATGCCG	172
Db	311	GGTTGACCCAGAAACAAAGCAATGCCAGAAAACGTTAAGTATGGATTGCTGGATGCCG	370
Qy	173	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG	232
Db	371	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG	430
Qy	233	GCTGTGTGTCATCAAGTAGAAGAAATGAGGGTTAAAGCTCTGGAATCTCAAAATTTGTTTC	292
Db	431	GCGTGGTGTCATCAAGTAGAAGAAATGAGGGTTAAAGCTCTGGAATCTCAAAATTTGTTTC	490

Qy	293	AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGTCATGGAAAGAGCTAGGGAGTGA	352
Db	491	AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGTCATGGAAAGAGCTAGGGAGTGA	550
Qy	353	TTTCCAAGGTCCAGACACAAAGAGACACCGGTTTACTCTGGAGCCACGGCAGGATGCGGT	412
Db	551	TTTCCAAGGTCCAGACACCAAGAGACACCGGTTTACTCTGGAGCCACGGCAGGATGCGGT	610
Qy	413	TGCTCAGGATGGAAGTGAAGTGGGAGACAGAGGTTCTGGATGTGTGGTGGAGAGGAGCC	472
Db	611	TGCTCAGGATGGAAGTGAAGTGGGAGACAGAGGTTCTGGATGTGTGGTGGAGAGGAGCC	670
Qy	473	TCAGCAAATACCCCTTTTGAATCTCCAGGGTGCAGAGTCAATTAAGTCCCAAGAGGAGGTG	532
Db	671	TCAGCAAATACCCCTTTTGAATCTCCAGGGTGCAGAGTCAATTAAGTCCCAAGAGGAGGTG	730
Qy	533	CCTATGGCTGGATTAATCAATCTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGTGTGT	592
Db	731	CCTATGGCTGGATTAATCAATCTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGTGTGT	790
Qy	593	TCAGCATAGTCCCATATGAAACCAATTAATCAAGAAACCTTTTGGAGCTTTGGACCTTGGG	652
Db	791	TCAGCATAGTCCCATATGAAACCAATTAATCAAGAAACCTTTTGGAGCTTTGGACCTTGGG	850
Qy	653	GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG	712
Db	851	GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG	910
Qy	713	CTCTGCAATTTTGGCTCTATGGCAAGGACTACAATGTCTACACATAGTCTTCTGTGCT	772
Db	911	CTCTGCAATTTTGGCTCTATGGCAAGGACTACAATGTCTACACATAGTCTTCTGTGCT	970
Qy	773	ATGGAAGGATCAGGACCTCTGGCAGAACTCGCCAAAGGACATTCAGTTTGAAGTAATG	832
Db	971	ATGGAAGGATCAGGACCTCTGGCAGAACTCGCCAAAGGACATTCAGTTTGAAGTAATG	1030
Qy	833	AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAGTACC	892
Db	1031	AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAGTACC	1090
Qy	893	TTTACAAGACCCCTTGCCACAAAGAGATTGAGATGACTCTTCATTCACAGCAGTTTGAA	952
Db	1091	TTTACAAGACCCCTTGCCACAAAGAGATTGAGATGACTCTTCATTCACAGCAGTTTGAA	1150
Qy	953	TCCAGGTTATGGAACATATCAACATGCAATCAAGACATCTGGAAGTCTTCAACACCA	1012
Db	1151	TCCAGGTTATGGAACATATCAACATGCAATCAAGACATCTGGAAGTCTTCAACACCA	1210
Qy	1013	GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCCACATCCAGGGG	1072
Db	1211	GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCCACATCCAGGGG	1270
Qy	1073	ATTTTGGGCAATTTTCAAGTTTACTTTTGTGATGAAGTTTAACTTTGACATCAGAGA	1132
Db	1271	ATTTTGGGCAATTTTCAAGTTTACTTTTGTGATGAAGTTTAACTTTGACATCAGAGA	1330
Qy	1133	AGTCTCTCAGAAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTTGGAGG	1192
Db	1331	AGTCTCTCAGAAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTTGGAGG	1390
Qy	1193	AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTCTG	1252
Db	1391	AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTCTG	1450
Qy	1253	GTACCTACATCTCTCCCTCTCTGTCGAAAGGCTATCATTTTACAGCTGATTCCTGGAGC	1312
Db	1451	GTACCTACATCTCTCCCTCTCTGTCGAAAGGCTATCATTTTACAGCTGATTCCTGGAGC	1510
Qy	1313	ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACGCCGCTGGACTTTGGGCTACATGC	1372
Db	1511	ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACGCCGCTGGACTTTGGGCTACATGC	1570
Qy	1373	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA	1432



Db 1571 TGAACTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACACCTCTCTCCCACTCCA 1630  
Qy 1433 CCTA 1436  
Db 1631 CCTA 1634

RESULT 9

US-10-240-965-242  
; Sequence 242, Application US/10240965  
; Publication No. US20030165924A1  
; GENERAL INFORMATION:  
; APPLICANT: INCITE GENOMICS, INC.  
; APPLICANT: SHIFFMAN, Dov  
; APPLICANT: SOMOGYI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEILHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; APPLICANT: TAI, Julie  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10/240,965  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/195,106  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; SEQ ID NO 242  
; LENGTH: 4411  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 3369  
; OTHER INFORMATION: Incyte ID No. US20030165924A1 347965.2  
US-10-240-965-242

Query Match 91.8%; Score 1319.2; DB 16; Length 4411;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 113 GTTCAACCCAGAACAAAGCATTCAGCAAGAAAGCTTAAGTATGGGATTTGCTGGATGCGG 172  
Db 184 GGTGACCCAGAACAAAGCATTCAGCAAGAAAGCTTAAGTATGGGATTTGCTGGATGCGG 243  
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGAGATGACACAG 232  
Db 244 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGAGATGACACAG 303  
Qy 233 GCGTGGTGATCAAGTAGAAGATCGAGGTTAAAGGTCCTGGAACTCTCAAAATTTGTTTC 292  
Db 304 GCGTGGTGATCAAGTAGAAGATCGAGGTTAAAGGTCCTGGAACTCTCAAAATTTGTTTC 363  
Qy 293 AGAAGTAAATGAATAGCATTTTACCTGATGATGATGATGATGATGATGATGATGATGATG 352  
Db 364 AGAAGTAAATGAATAGCATTTTACCTGATGATGATGATGATGATGATGATGATGATGATG 423  
Qy 353 TTCCAAGTTCAGCAGCAAGAGACACCGCTTTTACCTGGAGCCAGCGCATGCGGT 412  
Db 424 TTCCAAGTTCAGCAGCAAGAGACACCGCTTTTACCTGGAGCCAGCGCATGCGGT 483  
Qy 413 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGGTTCTGGATGTTGGAGAGAGGCC 472  
Db 484 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGGTTCTGGATGTTGGAGAGAGGCC 543  
Qy 473 TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGATCATTTACTGCGCAAGAGGAGTG 532  
Db 544 TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGATCATTTACTGCGCAAGAGGAGTG 603

Qy 533 CCTATGGCTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAACAAGTGCT 592  
Db 604 CCTATGGCTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAACAAGTGCT 663  
Qy 593 TCAGCATAGTCCCATATGAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 652  
Db 664 TCAGCATAGTCCCATATGAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 723  
Qy 653 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCAGTCCCGAGATAATG 712  
Db 724 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCAGTCCCGAGATAATG 783  
Qy 713 CTCTGCAATTTGCGCTCTATGSCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 772  
Db 784 CTCTGCAATTTGCGCTCTATGSCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 843  
Qy 773 ATGSGAAGGATCAGGCACCTCTGGGAGAAATCGGCCAAGACATTCAGGTTGCAAGTAATG 832  
Db 844 ATGSGAAGGATCAGGCACCTCTGGCAGAAATCGGCCAAGACATTCAGGTTGCAAGTAATG 903  
Qy 833 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACGTAAGTGACC 892  
Db 904 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACGTAAGTGACC 963  
Qy 893 TTTCAAGACCCCTTGCCACCAAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA 952  
Db 964 TTTCAAGACCCCTTGCCACCAAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA 1023  
Qy 953 TCCAGGGTATTTGGAAACTATCAACATGCCATCAAAGCATCTCTGAGCTCTTCAACACCA 1012  
Db 1024 TCCAGGGTATTTGGAAACTATCAACATGCCATCAAAGCATCTCTGAGCTCTTCAACACCA 1083  
Qy 1013 GTTACTGCCCTTACTCTCCAGTGTGCTTCAATGGATTTCTTGGCCACCATCCAGGGGG 1072  
Db 1084 GTTACTGCCCTTACTCTCCAGTGTGCTTCAATGGATTTCTTGGCCACCATCCAGGGGG 1143  
Qy 1073 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1132  
Db 1144 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1203  
Qy 1133 AAGTCTCTCAGGAAAGGTGACTGAGATGATGATGATGATGATGATGATGATGATGATG 1192  
Db 1204 AAGTCTCTCAGGAAAGGTGACTGAGATGATGATGATGATGATGATGATGATGATGATG 1263  
Qy 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGATGATGATGATGATGATGATG 1252  
Db 1264 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGATGATGATGATGATGATGATG 1323  
Qy 1253 GTACTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTCAAGCTGATTTCTCTGGAGC 1312  
Db 1324 GTACTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTCAAGCTGATTTCTCTGGAGC 1383  
Qy 1313 ACATCCATTTCTGCAAGATCCAGGACGCGCGGTGAGCTGAGCTGAGCTGAGCTGAGCTG 1372  
Db 1384 ACATCCATTTCTGCAAGATCCAGGACGCGCGGTGAGCTGAGCTGAGCTGAGCTGAGCTG 1443  
Qy 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1432  
Db 1444 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1503  
Qy 1433 CCTA 1436  
Db 1504 CCTA 1507

RESULT 10  
US-10-934-998-147/c  
; Sequence 147, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE



; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; FILE REFERENCE: BMA-04-1206  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 147  
; LENGTH: 704  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-934-998-147

Query Match 44.6%; Score 640.2; DB 22; Length 704;  
Best Local Similarity 99.5%; Pred. No. 1.6e-192;  
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 792 CTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCATG 851  
Db |||||||  
QY 704 CTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCATG 645  
Db |||||||  
QY 852 CTTTCATCTCGATATAAAGAGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCAC 911  
Db |||||||  
QY 644 CTTTCATCTCGATATAAAGAGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCAC 585  
Db |||||||  
QY 912 CAAGAGATTGAGATGACTCTTCATTCAGGAGTTTGAATCCAGGGTATTTGGAACATA 971  
Db |||||||  
QY 584 CAAGAGATTGAGATGACTCTTCATTCAGGAGTTTGAATCCAGGGTATTTGGAACATA 525  
Db |||||||  
QY 972 TCAACAAATGCAATCAAGGATCTGGAGCTTTCAACACAGTTACTGCCCTTACTCCCA 1031  
Db |||||||  
QY 524 TCAACAAATGCAATCAAGGATCTGGAGCTTTCAACACAGTTACTGCCCTTACTCCCA 465  
Db |||||||  
QY 1032 GTGTGCTTCAATGGGATTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTCAGC 1091  
Db |||||||  
QY 464 GTGTGCTTCAATGGGATTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTCAGC 405  
Db |||||||  
QY 1092 TTTTACTTTTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGT 1151  
Db |||||||  
QY 404 TTTTACTTTTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGT 345  
Db |||||||  
QY 1152 GACTGAGATGATAAAGTTCTGCTCAGCCCTGGGAGGAGATAAAACATCTTTACGC 1211  
Db |||||||  
QY 344 GACTGAGATGATAAAGTTCTGCTCAGCCCTTGAGGGAGATAAAACATCTTTACGC 285  
Db |||||||  
QY 1212 TGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTGGTACCTACATTTCTCCCT 1271  
Db |||||||  
QY 284 TGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTGGTACCTACATTTCTCCCT 225  
Db |||||||  
QY 1272 CTTTCTGCAAGGCTATCATTTTCAAGTGTATTCCTGGGAGCAATCCATTTTCAATGGCAA 1331  
Db |||||||  
QY 224 CTTTCTGCAAGGCTATCATTTCAAGTGTATTCCTGGGAGCAATCCATTTTCAATGGCAA 165  
Db |||||||  
QY 1332 GATCCAGGGCAGGACGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGAT 1391  
Db |||||||  
QY 164 GATCCAGGGCAGGACGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGAT 105  
Db |||||||  
QY 1392 CCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACCTA 1436  
Db |||||||  
QY 104 CCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACCTA 60  
Db |||||||

RESULT 11  
US-10-934-998-193/c  
; Sequence 193, Application US/10934998  
; Publication No. US20050153917A1

; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 193  
; LENGTH: 6164  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-934-998-193

Query Match 44.6%; Score 640.2; DB 22; Length 6164;  
Best Local Similarity 99.5%; Pred. No. 6e-192;  
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 792 CTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCATG 851  
Db |||||||  
QY 1811 CTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCATG 1752  
Db |||||||  
QY 852 CTTTCACTCTGATATAAAGAGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCAC 911  
Db |||||||  
QY 1751 CTTTCACTCTGATATAAAGAGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCAC 1692  
Db |||||||  
QY 912 CAAGAGATTGAGATGACTCTTCATTCAGCAGATTTGAAATCCAGGGTATTTGGAACATA 971  
Db |||||||  
QY 1691 CAAGAGATTGAGATGACTCTTCATTCAGCAGATTTGAAATCCAGGGTATTTGGAACATA 1632  
Db |||||||  
QY 972 TCAACAAATGCAATCAAGGATCTGGAGCTTTCAACACAGTTACTGCCCTTACTCCCA 1031  
Db |||||||  
QY 1631 TCAACAAATGCAATCAAGGATCTGGAGCTTTCAACACAGTTACTGCCCTTACTCCCA 1572  
Db |||||||  
QY 1032 GTGTGCTTCAATGGGATTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTCAGC 1091  
Db |||||||  
QY 1571 GTGTGCTTCAATGGGATTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTCAGC 1512  
Db |||||||  
QY 1092 TTTTACTTTTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGT 1151  
Db |||||||  
QY 1511 TTTTACTTTTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGT 1452  
Db |||||||  
QY 1152 GACTGAGATGATAAAGTTCTGCTCAGCCCTGGGAGGAGATAAAACATCTTTACGC 1211  
Db |||||||  
QY 1451 GACTGAGATGATAAAGTTCTGCTCAGCCCTGGGAGGAGATAAAACATCTTTACGC 1392  
Db |||||||  
QY 1212 TGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTCTGGTACCTACATTTCTCCCT 1271  
Db |||||||  
QY 1391 TGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTCTGGTACCTACATTTCTCCCT 1332  
Db |||||||  
QY 1272 CTTTCTGCAAGGCTATCATTTTCAAGTGTATTCCTGGGAGCAATCCATTTTCAATGGCAA 1331  
Db |||||||  
QY 1331 CTTTCTGCAAGGCTATCATTTCAAGTGTATTCCTGGGAGCAATCCATTTTCAATGGCAA 1272  
Db |||||||  
QY 1332 GATCCAGGGCAGGACGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGAT 1391  
Db |||||||  
QY 1271 GATCCAGGGCAGGACGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGAT 1212  
Db |||||||  
QY 1392 CCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACCTA 1436  
Db |||||||  
QY 1211 CCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACCTA 1167  
Db |||||||

RESULT 12

```
US-09-918-995-24656
; Sequence 24656, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24656
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-24656

Query Match      28.8%; Score 414; DB 10; Length 475;
Best Local Similarity 96.6%; Pred. No. 1.5e-120;
Matches 423; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 665 AAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCAAGATATGCTCTGCAATTTC 724
DB 38 AGGGCACTTTATGTATACCCCTTAACCAAGACTATCGAGTCCCAAGATATGCTCTGCAATTTC 97
QY 725 GCCTCTATGGCAAGGACTACAATGTCTACACATAGTCTTGTGCTATGGGAAGATC 784
DB 98 ACTCTATGGCAGGACTACAATGTCTACACATAGTCTTGTGCTATGGGAAGATC 157
QY 785 AGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAAATGAAATTTTCAGGG 844
DB 158 ATGCACTCTGGCATAAATCGGCAAGGACATTCAGGTTGCAAGTAAATGAAATCTCAGGG 217
QY 845 ACCCATGCTTTATCTCGATATAGAAGGTAGTGAACGTAAAGTGAACCTTTACAGACCC 904
DB 218 ACCCATGCTTTATCTCGATATAGAAGGTAGTGAACGTAAAGTGAACCTTTACAGACCC 277
QY 905 CTGCAACCAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATG 964
DB 278 CTGCAACCAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATG 337
QY 965 GAACTATCAACAATGCCATCAAGCATCTCGAGCTTTCAACACCAAGTAACTGCGCTT 1024
DB 338 GAACTATCAACAATGCCATCAAGCATCTCGAGCTTTCAACACCAAGTAACTGCGCTT 397
QY 1025 ACTCCAGTGCCTTCAATGGATTTCTTCCACCACTCCAGGGGATTTTGGGGCAT 1084
DB 398 ACTCCAGTGCCTTCAATGGATTTCTTCCACCACTCCAGGGGATTTTGGGGCAT 457
QY 1085 TTTTCACTTTTACTTTG 1102
DB 458 TTTTCACTTTTACTTTG 475

RESULT 13
US-09-918-995-23052
; Sequence 23052, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23052

US-09-918-995-23052
; Sequence 23052, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathan M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
; CURRENT APPLICATION NUMBER: US/10/002,631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275
; LENGTH: 703
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (656)...(698)
; OTHER INFORMATION: n = A, C, G, or T
US-10-002-631C-275

Query Match      23.4%; Score 335.8; DB 16; Length 703;
Best Local Similarity 80.2%; Pred. No. 1.6e-95;
Matches 394; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 118 ACCCAGAACAAAGCATTTGCCAGAAACCGTTAAGTATGGGATTTGCTCGATCGCGGTCT 177
|||||
```

Db 547 ACCAGAACAAACCTTTGGCAGAAAATGTTAAGTATGGGATTGTGTGGATGCGGGTCA 488  
Qy 178 TCTCACAAAGTTTATACATCTATTAAGTGGCCAGCAGAGAAAAGAGAAATGACACAGCGGTG 237  
Db 487 TCTCACAAACCTGTACATCTACAAGTGGCCGCGGAGAGAGAAATGACACAGGGGTG 428  
Qy 238 GTGCATCAAGTAGAAGATGSCAGGTTTAAAGTTCCTTGGAAATCTCAAAAATTTGTTACAGAAA 297  
Db 427 GTGCAGAGTTAGAGAAATGCCAAGTGAAGGTCCTTGGAAATCTCAAAAATATGCTCAGAAA 368  
Qy 298 GTAATGAATAGGCAATTTTACCTGACTGATTTGATGTAAGAGAGCTTAGGAAAGTGAATCCA 357  
Db 367 ACAGATGAATCGGTGCTACCTTGGCCGAATGCAATGGAATCTGTCACCCAGAACTGATACCA 308  
Qy 358 AGTCCAGCAGCACAGACACCCGTTTACCTGGAGCCACGCCAGGCATGCGGTTGCTC 417  
Db 307 ACATCCAAGCATCACAGATCTCTGTCTACCTGGAGCCACAGCAGGCATGCGCTTGTCTT 248  
Qy 418 AGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGCTGGTGGAGAGGAGCCTCAGC 477  
Db 247 AGAATGGAAGCGAACAATCGGCAGACGAGGTCCTGGCTGAGTGTCAACAAGCCTTAAG 188  
Qy 478 AACTACCCCTTTGACTTCCAGGCTGCCAGGATCAATTAAGTCCAGAGGAAGGTGCTTAT 537  
Db 187 AGCTACCCCTTTGACTTCCAGGCTGCCAAGATCATCACTGGACAAGGAAGGTGCTTAT 128  
Qy 538 GGCTGGAATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGTTTACG 597  
Db 127 GGCTGGAATTAATCAACTATCTGCTGGGCAGATTCACTCAGGAACAGAGTTGGCTTAAGC 68  
Qy 598 ATAGTCCCATTA 608  
Db 67 CTCAATCTCAGA 57

## RESULT 15

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; Sequence 3, Application US/09923304  
; Patent No. US20020081612A1  
; GENERAL INFORMATION:  
; APPLICANT: KATZ, RUTH  
; APPLICANT: JIANG, FENG  
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS  
; FILE REFERENCE: UTSC-658US  
; CURRENT APPLICATION NUMBER: US/09/923, 304  
; CURRENT FILING DATE: 2001-08-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1672)  
US-09-923-304-3

Query Match 20.3%; Score 291; DB 9; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 7e-81;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

Qy 120 CAGAACAAAGCATTCGCAGAAAACGTTAAGTAGTGGATTGCTCTGGATGCGGGTCTTTC 179  
Db 220 CAAGCAAGAGGTCTCCCTCCAGGACTGAAGTAGTATGTTGCTGGATGCGGGTCTTTC 279  
Qy 180 TCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAAATGACACAGCGGTGCT 239  
Db 280 AAGAACCAAGTCTAGTGTATCAATGGCCAGCAGAAAAGAGAAATATACCGAGTGGT 339  
Qy 240 GCATCAAGTAGAAGATGCAAGGTTAAAGGTCTCTGGAATCTCAAAATTTGTTACAGAAAGT 299  
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Qy 360 GTCCAGACCAAGAAGACACCCGTTTAACTGGAGCCACGGCAGGATCGCGTTGCTCAG 419  
Db 460 CCACCTCCACGGATCCACCCCATTTACCTGGAGCCACGGCTGGGATCGCGTTGCTGAG 519  
Qy 420 GATGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCTCAGCAA 479  
Db 520 GTTGCAAAATGAACAGCAGCTAAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC 579  
Qy 480 CTACCCCTTTGACTTCCAGGCTGCCAGGATCAATTAAGTGGCCCAAGAGAAAGGTGCTTATGG 539  
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Qy 540 CTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTTCAGAAAAACAAGGTGTTTCAAGAT 599  
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Qy 600 AGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGGAGCCTC 659  
Db 700 GGTGC-----ACCCGCAATGGAGTGGAAACACGGGTGCCCTTGAAGTGGTGGCTTC 753  
Qy 660 TACAAAGTCACTTTGTACCCCAAAACCCAGACTATCGAGTCCCCAGATAATGCTCTGCA 719  
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Qy 780 GGATCAGGCACTCTGGCAGAAAACCTGCCNAAGACATTCAGGTTGCAAGTAATGAA--T 836  
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Qy 1068 GGGGATTTTGGGCATTTTTCAGCTTTTTCATTTGTGATGAAGTTTAAACTTGACATC 1127  
Db 1174 AGGGCCATTTTGGGCTTTTTCAGGATTTCTACTACACAGCCAGTGTCTTTAAATCT---TTC 1230  
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Qy 1368 CATGCTGAACCTGACCAACATGATCCAGCTCAGCAACCATTTG 1410

Db 1471 CATGCTCAGCCTGACCAACCAAGATCCAGCTGAAAGCCCTCTG 1513

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